

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 1, 2001, 11:42:49 ; Search time 11.61 Seconds  
(without alignments) 563.548 Million cell updates/sec

Title: US-09-479-252-1\_COPY\_91\_281

Perfect score: 996  
Sequence: 1 MILPTSEETISTVQEKQONI.....NEHLIDMDHEASFGAFLVG 191

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 segs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SWISSPROT\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 996   | 100.0       | 281    | 1  | TNF10_HUMAN |
| 2          | 693   | 69.6        | 291    | 1  | TNF10_MOUSE |
| 3          | 235.5 | 23.6        | 316    | 1  | TNF11_MOUSE |
| 4          | 232.5 | 23.3        | 317    | 1  | TNF11_HUMAN |
| 5          | 188.5 | 18.9        | 279    | 1  | FASL_MOUSE  |
| 6          | 180   | 18.1        | 281    | 1  | FASL_HUMAN  |
| 7          | 177.5 | 17.8        | 278    | 1  | FASL_RAT    |
| 8          | 152   | 15.3        | 240    | 1  | TNF14_HUMAN |
| 9          | 142   | 14.3        | 261    | 1  | TNF5_BOVIN  |
| 10         | 136.5 | 13.7        | 235    | 1  | TNF5_BOVIT  |
| 11         | 134.5 | 13.5        | 204    | 1  | TNFB_PIG    |
| 12         | 132.5 | 13.3        | 234    | 1  | TNFA_CAYPO  |
| 13         | 130   | 13.1        | 232    | 1  | TNFA_PIG    |
| 14         | 129.5 | 13.0        | 235    | 1  | TNFA_PIG    |
| 15         | 128.5 | 12.9        | 260    | 1  | TNFB_BOVIN  |
| 16         | 127.5 | 12.8        | 204    | 1  | TNFB_BOVIN  |
| 17         | 126   | 12.7        | 234    | 1  | TNFA_HORSE  |
| 18         | 125   | 12.6        | 234    | 1  | TNFA_MARMO  |
| 19         | 125   | 12.6        | 260    | 1  | TNFB_FELCA  |
| 20         | 124.5 | 12.5        | 261    | 1  | TNFB_HUMAN  |
| 21         | 123   | 12.3        | 233    | 1  | TNFB_HUMAN  |
| 22         | 123   | 12.3        | 260    | 1  | TNFB_CANFA  |
| 23         | 122.5 | 12.3        | 229    | 1  | TNFA_CEREL  |
| 24         | 122   | 12.2        | 205    | 1  | TNFB_HUMAN  |
| 25         | 121   | 12.1        | 235    | 1  | TNFB_MOUSE  |
| 26         | 121   | 12.1        | 235    | 1  | TNFA_RAT    |
| 27         | 120   | 12.0        | 233    | 1  | TNFA_PAPSP  |
| 28         | 117.5 | 11.8        | 201    | 1  | TNFB_MACEU  |
| 29         | 117.5 | 11.8        | 234    | 1  | TNFA_SHEEP  |
| 30         | 117   | 11.7        | 233    | 1  | TNFA_MACMU  |
| 31         | 117   | 11.7        | 233    | 1  | TNFA_PAPHU  |
| 32         | 116.5 | 11.7        | 233    | 1  | TNFA_CANFA  |
| 33         | 116   | 11.6        | 233    | 1  | TNFA_MACFA  |

|    |       |      |     |   |            |        |              |
|----|-------|------|-----|---|------------|--------|--------------|
| 34 | 114   | 11.4 | 202 | 1 | TNFB_MOUSE | P09225 | mus musculus |
| 35 | 113.5 | 11.4 | 233 | 1 | TNFA_TRIYU | P79374 | trichosurus  |
| 36 | 112   | 11.2 | 233 | 1 | TNFA_BOVIN | O06599 | bos taurus   |
| 37 | 111.5 | 11.2 | 202 | 1 | TNFB_RAT   | O06332 | rattus norv  |
| 38 | 111   | 11.1 | 391 | 1 | EDA_MOUSE  | O54693 | mus musculus |
| 39 | 108.5 | 10.9 | 306 | 1 | TNFC_MOUSE | P41155 | mus musculus |
| 40 | 108   | 10.8 | 193 | 1 | TNFA_CAPHI | P13296 | capra hircu  |
| 41 | 108   | 10.8 | 233 | 1 | TNFA_MACEU | O77764 | macropus eu  |
| 42 | 107   | 10.7 | 197 | 1 | TNFB_RABIT | P10154 | oryctolagus  |
| 43 | 106   | 10.6 | 391 | 1 | EDA_HUMAN  | O92838 | homo sapien  |
| 44 | 102   | 10.2 | 244 | 1 | TNFC_HUMAN | O06643 | homo sapien  |
| 45 | 98.5  | 9.9  | 233 | 1 | TNFA_FELCA | P19101 | felis silve  |

## ALIGNMENTS

| RESULT      | 1  | STANDARD | PRT | 281 AA. |
|-------------|--|----------|-----|---------|
| TNF10_HUMAN |  |          |     |         |
| ID          | TNF10_HUMAN  |          |     |         |
| AC          | P50591   |          |     |         |
| DT          | 01-OCT-1996 (Rel. 34, Created)   |          |     |         |
| DT          | 01-OCT-1996 (Rel. 34, Last sequence update)  |          |     |         |
| DT          | 01-OCT-2000 (Rel. 40, Last annotation update)  |          |     |         |
| DE          | TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 10 (TNF-RELATED APOPTOSIS INDUCING LIGAND) (TRAIL PROTEIN) (APO-2 LIGAND) (APO-2L).  |          |     |         |
| GN          | TNFSF10 OR TRAIL OR APO2L.   |          |     |         |
| OS          | Homo sapiens (human).  |          |     |         |
| OC          | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  |          |     |         |
| OC          | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  |          |     |         |
| OX          | NCBI_Taxid=9606;   |          |     |         |
| RN          | [1]  |          |     |         |
| RP          | SEQUENCE FROM N.A.   |          |     |         |
| RX          | MEDLINE=96111955; PubMed=8777713;  |          |     |         |
| RA          | Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,   |          |     |         |
| RA          | Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,   |          |     |         |
| RA          | Goodwin R.G.;  |          |     |         |
| RT          | "Identification and characterization of a new member of the TNF family that induces apoptosis."  |          |     |         |
| RT          | Immunoty 3:673-682(1995).  |          |     |         |
| RL          | [2]  |          |     |         |
| RN          | SEQUENCE FROM N.A.   |          |     |         |
| RP          | TISSUE=Placenta;   |          |     |         |
| RC          | MEDLINE=96278649; PubMed=8663110;  |          |     |         |
| RX          | Pitti R.M., Masters S.A., Ruppert S., Donahue C.J., Moore A.,  |          |     |         |
| RA          | Askenazi A.;   |          |     |         |
| RT          | "Induction of apoptosis by Apo-2 ligand, a new member of the tumor necrosis factor cytokine family."   |          |     |         |
| RT          | J. Biol. Chem. 271:12687-12690(1996).  |          |     |         |
| CC          | -1- FUNCTION: INDUCES APOPTOSIS.   |          |     |         |
| CC          | -1- SUBUNIT: HOMODIMER (POTENTIAL).  |          |     |         |
| CC          | -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).  |          |     |         |
| CC          | -1- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG AND PROSTATE.   |          |     |         |
| CC          | -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.   |          |     |         |
| CC          | -----  |          |     |         |
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| CC          | -----  |          |     |         |
| CC          | EMBL: U37518; AAC50332.1; -  |          |     |         |
| CC          | EMBL: U57059; AAB01233.1; -  |          |     |         |
| CC          | DR MIM: 603598; -  |          |     |         |
| CC          | DR InterPro: IPR000478; -  |          |     |         |
| CC          | DR Pfam: PF00229; TNF_1;   |          |     |         |
| CC          | DR PROSITE: PS00251; TNF_1;  |          |     |         |
| CC          | DR PROSITE: PS50049; TNF_2; 1.   |          |     |         |
| CC          | DR CytoKine: Transmembrane; Signal-anchor; Apoptosis.  |          |     |         |
| CC          | FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).  |          |     |         |

FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
 FT DOMAIN 39 281 EXTRACELLULAR (POTENTIAL).  
 SQ SEQUENCE 281 AA: 32509 MW: DDAAF78DAAB2P6D CRC64:

Query Match 100.0%; Score 996; DB 1; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 1,le-78;  
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLRTSEETISTVOEKQONISPLVREGRPOVAHAITGTGRSNTLSPNSKNEKALGRK 60  
 |||  
 DB 91 MLRTSEETISTVOEKQONISPLVREGRPOVAHAITGTGRSNTLSPNSKNEKALGRK 150  
 |||  
 OY 61 INSWESSRSGHSLNLHRLNGELVYHEKGFYIYSQTYFRFOEIKENTKNDKQVQYI 120  
 |||  
 DB 151 INSWESSRSGHSLNLHRLNGELVYHEKGFYIYSQTYFRFOEIKENTKNDKQVQYI 210  
 |||  
 OY 121 YKTSYDPDPLILMKSRNSCMSKDAEYGLYSYOGGIFELKENDRIFVSTNHLDMH 180  
 |||  
 DB 211 YKTSYDPDPLILMKSRNSCMSKDAEYGLYSYOGGIFELKENDRIFVSTNHLDMH 270  
 |||  
 OY 181 EASFEGAFVVG 191  
 |||  
 DB 271 EASFEGAFVVG 281

## RESULT 2

TN10\_MOUSE STANDARD; PRT: 291 AA.

AC P50592;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 10 (TNF-RELATED  
 APPOPTOSIS INDUCING LIGAND) (TRAIL PROTEIN).  
 GN TNFSF10 OR TRAIL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=96111955; PubMed=8777713;  
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,  
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,  
 RA Goodwin R.G.;  
 RT \*Identification and characterization of a new member of the TNF  
 RT family that induces apoptosis.\*;  
 RL Immunity 3:673-682(1993).  
 CC -1- FUNCTION: INDUCES APOPTOSIS.  
 CC -1- SUBUNIT: HOMOTRIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: WIDESPREAD.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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DR EMBL: U37522; AAC52345.1;  
 DR MGD: MGI:107414; Tnfsf10.  
 DR InterPro: IPR000478;  
 DR Pfam: PF00229; TNF\_1;  
 DR PROSITE: PS00251; TNF\_1;  
 DR PROSITE: PS50049; TNF\_2; 1.  
 KW Cytokine; Transmembrane; Signal-anchor; Apoptosis.  
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 18 17 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
 FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).

FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 291 AA: 33477 MW: 3FEACAB9FD7802 CRC64:

Query Match 69.6%; Score 693; DB 1; Length 291;  
 Best Local Similarity 69.1%; Pred. No. 1,3e-52;  
 Matches 134; Conservative 23; Mismatches 31; Indels 6; Gaps 1;

OY 3 LRTESEETISTVOEKQONISPLVREGRPOVAHAITGTGRSNTLSPNSKNEKALGRKIN 62  
 |||  
 DB 97 LRTESEETISTVOEKQONISPLVREGRPOVAHAITGTGRSNTLSPNSKNEKALGRK 156  
 |||  
 OY 63 INSWESSRSGHSLNLHRLNGELVYHEKGFYIYSQTYFRFOEIKENTKNDKQVQYI 116  
 |||  
 DB 157 INSWESSRSGHSLNLHRLNGELVYHEKGFYIYSQTYFRFOEIKENTKNDKQVQYI 216  
 |||  
 OY 117 VOYIYKTSYDPDPLILMKSRNSCMSKDAEYGLYSYOGGIFELKENDRIFVSTNHLDMH 176  
 |||  
 DB 217 VOYIYKTSYDPDPLILMKSRNSCMSKDAEYGLYSYOGGIFELKENDRIFVSTNHLDMH 276  
 |||  
 OY 177 DMDEASFEGAFV 190  
 |||  
 DB 277 DMDEASFEGAFV 290

## RESULT 3

TN11\_MOUSE STANDARD; PRT: 316 AA.

AC O35235; O35306;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11 (RECEPTOR ACTIVATOR  
 OF NUCLEAR FACTOR KAPPA B LIGAND) (RANKL) (TNF-RELATED ACTIVATION-  
 INDUCED CYTOKINE) (TRANCE) (OSTEOPROTEGERIN LIGAND) (OPG) (OSTEOCLAST  
 DIFFERENTIATION FACTOR) (ODF) (OSTEOCLASTOGENESIS-INHIBITORY FACTOR)  
 DE (OCIF).  
 GN TNFSF11 OR RANKL OR TRANCE OR OPG.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=HydrIdoma;  
 RX MEDLINE=97460112; PubMed=9312132;  
 RA Wong B.R., Rho J., Aron J., Robinson E., Orlinick J., Chao M.,  
 RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,  
 RA Choi Y.;  
 RT \*TRANCE is a novel ligand of the tumor necrosis factor receptor family  
 RT that activates c-Jun N-terminal kinase in T cells.\*;  
 RL J. Biol. Chem. 272:25190-25194(1997).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC TISSUE=bone marrow;  
 RX MEDLINE=98227661; PubMed=9568710;  
 RA lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,  
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,  
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,  
 RA Boyle W.J.;  
 RT \*Osteoprotegerin ligand is a cytokine that regulates osteoclast  
 RT differentiation and activation.\*;  
 RL Cell 93:165-176(1998).

RP SEQUENCE FROM N.A.  
 RC TISSUE=bone marrow; stroma;  
 RX MEDLINE=9818248; PubMed=9520411;  
 RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M.,  
 RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,  
 RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;  
 RT \*Osteoclast differentiation factor is a ligand for  
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical

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RT      to "TRANSE/RANKL.":
RL      Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN      [4]
RP      SEQUENCE FROM N.A.
RC      TISSUE-Thymic Lymphoma;
RX      MEDLINE=98032977; Pubmed=9367155;
RA      Anderson D.M., Maraskovsky E., Billingsley W.L., Douall W.C.,
RA      Tomelesko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA      Galibert L.;
RT      "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT      and dendritic-cell function.";
RL      Nature 390:175-179(1997).
RP      [5]
RP      SEQUENCE FROM N.A.
RA      Ikeda T.;
RL      Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
CC      -1- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC      ARGUMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
CC      PROLIFERATION, MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
CC      BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC      REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.
CC      -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
CC      -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT
CC      NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS
CC      BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE
CC      TRABECULAR BONE AND LUNG.
CC      -1- DISEASE: DEFICIENCY IN TNFSF11 RESULTS IN FAILURE TO FORM LOBULO-
CC      ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH
CC      OF NEONBORN. TRANS-DEFICIENT MICE SHOW SEVERE OSTEOPELOSIS, WITH
CC      NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT
CC      PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING
CC      THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,
CC      WITH THICK, IRRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN
CC      HYPERTROPHIC CHONDROCYTES.
CC      -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC      -----
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL; AF013173; AAC40113.1; -
DR      EMBL; AF013170; AAC71061.1; -
DR      EMBL; AB008426; BAA25425.1; -
DR      EMBL; AF019048; AAB68122.1; -
DR      EMBL; AB036798; BAA97259.1; -
DR      MGD; MGI:1100089; Tnfstf11.
DR      InterPro; IPR000478; -
DR      InterPro; IPR003263; -
DR      Pfam; PF00229; TNF; 1.
DR      PROSITE; PS00251; TNF_1; FALSE_NEG.
DR      PROSITE; PS50045; TNF_2; 1.
KW      Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW      Signal-anchor.
FT      DOMAIN 1 48 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 49 69 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT      FT
FT      DOMAIN 70 316 EXTRACELLULAR (POTENTIAL).
FT      CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CONFLICT 99 99 G -> D (IN REF. 4).
SO      SEQUENCE 316 AA; 34944 MW; 08DF63A2BE00967A CRC64;

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|        |  |   |                         |
|--------|--|---|-------------------------|
| Db     | 107  | SEDLPDSCRMKQAFGAVQKELQHTIV-----GQRRSGAPAMMESGMLDVAQRKPE       | 160                     |
| Oy     | 34   | -----AHITTRGNSNTLSPNSKNEKALGKINSWESSGSHFSLNHLRNGELVIEHK       | 89                      |
| Db     | 161  | AQPPAHLT-----INASISIGSGHKYTL-----SSWYHDR-GNAKISSNMTLSNGKLRVND | 210                     |
| Oy     | 90   | GFFYYISQOTFRFQPELKEKNTKDKOMVOYIKYT--SYDPDPLLKSAANSQMSMDATYG   | 148                     |
| Db     | 211  | GFFVLYANICRHHETSGSVPTIYLDLIMVYVTSIKTIPSSHNLKMGKSTKNWSGNSSEFH  | 270                     |
| Oy     | 149  | LYSIYGGIFELKENDRIEFSVSTNEHLIDMDHASEFGFAFLV                    | 190                     |
| Db     | 271  | FYSINVGFFELKRGEEISIQVSNPSLDDPDQDATYFGAFKV                     | 312                     |
| RESULT | 4  |   |                         |
| TN11   | HUMAN  | STANDARD:   | PRT: 317 AA.            |
| AC     | 014788:  | 014723:   | Q9P2Q3:                 |
| DT     | 01-OCT-2000  | (Rel. 40,   | Created)                |
| DT     | 01-OCT-2000  | (Rel. 40,   | Last sequence update)   |
| DT     | 01-OCT-2000  | (Rel. 40,   | Last annotation update) |
| DE     | TUMOR NECROSIS FACTOR LIAND SUPERFAMILY MEMBER 11 (RECEPTOR ACTIVATOR  |   |                         |
| DE     | OF NUCLEAR FACTOR KAPPA B LIAND) (RANKL) (TNF-RELATED ACTIVATION-      |   |                         |
| DE     | INDUCED CYTOKINE) (TRANCE) (OSTEOPROTEGERIN LIAND) (OPGL) (OSTEOCLAST  |   |                         |
| DE     | DIFFERENTIATION FACTOR) (ODF).   |   |                         |
| GN     | TNFSF11 OR RANKL OR TRANCE OR OPGL.                                    |   |                         |
| OS     | Homo sapiens (Human).  |   |                         |
| OC     | Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;      |   |                         |
| OC     | Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.            |   |                         |
| OX     | NCBI_TaxID=9606;   |   |                         |
| RN     | [1]  |   |                         |
| RP     | SEQUENCE FROM N.A.   |   |                         |
| RC     | TISSUE=Bone marrow, and Peripheral blood;                              |   |                         |
| RX     | MEDLINE=98032977; PubMed=9367155;                                      |   |                         |
| RA     | Anderson D.M., Maraskovsky E., Billingsley W.L., Douglall W.C.,        |   |                         |
| RA     | Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,          |   |                         |
| RA     | Gallibert L.;  |   |                         |
| RT     | "A homolog of the TNF receptor and its ligand enhance T-cell growth    |   |                         |
| RT     | and dendritic-cell function.";   |   |                         |
| RL     | Nature 390:175-179(1997).  |   |                         |
| RN     | [2]  |   |                         |
| RP     | SEQUENCE FROM N.A.   |   |                         |
| RC     | TISSUE=Lymph node;   |   |                         |
| RX     | MEDLINE=98227661; PubMed=9568710;                                      |   |                         |
| RA     | laeey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,            |   |                         |
| RA     | Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,   |   |                         |
| RA     | Sullivan J., Hawkins T., Davy E., Capparelli C., Eli A., Qian Y.-X.,   |   |                         |
| RA     | Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,    |   |                         |
| RA     | Boyle W.J.;  |   |                         |
| RT     | "Osteoprotegerin ligand is a cytokine that regulates osteoclast        |   |                         |
| RT     | differentiation and activation.";                                      |   |                         |
| RL     | Cell 93:165-176(1998).   |   |                         |
| RN     | [3]  |   |                         |
| RP     | SEQUENCE OF 73-317 FROM N.A.   |   |                         |
| RC     | TISSUE=Tymocytes;  |   |                         |
| RX     | MEDLINE=97460112; PubMed=9312132;                                      |   |                         |
| RA     | Wong B.R., Rho J., Arron J., Robinson E., Orlickick J., Chao M.,       |   |                         |
| RA     | Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,   |   |                         |
| RA     | Choi Y.;   |   |                         |
| RT     | "TRANCE is a novel ligand of the tumor necrosis factor receptor family |   |                         |
| RT     | that activates c-Jun N-terminal kinase in T cells.";                   |   |                         |
| RL     | J. Biol. Chem. 272:25190-25194(1997).                                  |   |                         |
| RN     | [4]  |   |                         |
| RP     | SEQUENCE FROM N.A. (ISOFORM 2).  |   |                         |
| RC     | TISSUE=Tongue;   |   |                         |
| RX     | MEDLINE=20175237; PubMed=10708568;                                     |   |                         |
| RA     | Nagai M., Kyakumoto S., Sato N.;                                       |   |                         |
| RT     | "Cancer cells responsible for humoral hypercalcaemia express mRNA      |   |                         |
| RT     | encoding a secreted form of ODF/TRANCE that induces osteoclast         |   |                         |
| RT     | formation.";   |   |                         |
| RT     | Biochem. Biophys. Res. Commun. 269:532-536(2000).                      |   |                         |
| CC     | -I- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.        |   |                         |

| ID | FASTL_MOUSE                                   | STANDARD | PRT | 279 AA |
|----|---|----------|-----|--------|
| AC | P41047; Q61217; Q9RIE2;                       |          |     |        |
| DT | 01-FEB-1995 (Rel. 31, Created)                |          |     |        |
| DT | 01-FEB-1995 (Rel. 31, Last sequence update)   |          |     |        |
| DT | 01-OCT-2000 (Rel. 40, Last annotation update) |          |     |        |
| DE | FAS ANTIGEN LIGAND.                           |          |     |        |
| EN | TNFSF6 OR APRILG1 OR FASL OR GLD.             |          |     |        |

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090.  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM FASL).  
RX MEDLINE=94185175; PubMed=7511063;  
RA Takahashi T., Tanaka M., Brennan C.I., Jenkins N.A., Copeland N.G.,  
RA Suda T., Nagata S.,  
RT "Generalized lymphoproliferative disease in mice, caused by a point  
RT mutation in the Fas ligand.";  
RL Cell 76:969-976(1994).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.  
RC STRAIN=C57BL/6;  
RX MEDLINE=95388076; PubMed=7544870;  
RA Peltsch M.J., Tschopp J.J.;  
RT "Comparative molecular modelling of the Fas-ligand and other members  
RT of the TNF family.";  
RL Mol. Immunol. 32:761-772(1995).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM FASL).  
RX MEDLINE=95196085; PubMed=7889405;  
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,  
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;  
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a  
RT TNF family gene cluster.";  
RL Immunity 1:131-136(1994).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM FASL).  
RC STRAIN=BALB/C;  
RA Fenner M.H., Shida T., Isselbacher K.J.;  
RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in  
RT two amino acids.";  
RN Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM FASLS).  
RC STRAIN=C3H; TISSUE=Spleen;  
RX MEDLINE=20021694; PubMed=10552956;  
RA Ayrolid E., D'Adamo F., Zollo O., Agostini M., Moraca R.,  
RA Canmarile L., Migliorati G., Delfino D.V., Riccardi C.;  
RT "Cloning and expression of a short Fas ligand: A new alternatively  
RT spliced product of the mouse Fas ligand gene.";  
RL Blood 94:3456-3467(1999).  
RN [6]  
RP CHARACTERIZATION OF VARIANT GLD.  
RX MEDLINE=96091792; PubMed=7495745;  
RA Haime N., Peltsch M.C., Imler M., Schroeter M., Lowin B.,  
RA Rousseau M., Bron C., Renno T., French L., Tschopp J.;  
RT "Characterization of the non-functional Fas ligand of gld mice.";  
RL Int. Immunol. 7:1381-1386(1995).  
RN [7]  
RP FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT  
RC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN  
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.  
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF  
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE  
CC T CELLS, OR BOTH.  
CC [8]  
RP SUBUNIT: HOMODIMER (PROBABLE).  
CC [9]  
RP SUBCELLULAR LOCATION: ISOFORM FASL IS A TYPE II MEMBRANE PROTEIN.  
CC [10]  
RP ISOFORM FASLS IS SOLUBLE.  
CC [11]  
RP ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FASLS; ARE  
CC PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS  
CC WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL  
CC INTERACTION.  
CC [12]  
RP DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED  
CC LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE  
CC RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.  
CC [13]  
RP SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
CC [14]  
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CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION  
CC AT THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON  
CC ITS use BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO



SEQUENCE 281 AA: 31485 MW: A8A6EB358246E9BB CRC64;  
 Query Match 18.1%; Score 180; DB 1; Length 281;  
 Best Local Similarity 27.6%; Pred. No. 1.5e-08;  
 Matches 54; Conservative 36; Mismatches 66; Indels 40; Gaps 9;  
 QY 3 LRTSEETISTVQKQONT--SPLVNERGPORVAHITGTGRSNLTSSPNSKNEKALGR 59  
 DB 114 LRETSQMTASTASLEKQIHPSPPPEKKELRKVAHLT--GKSNRSMSP----- 159  
 QY 60 KINSWSSSGHSFSLNLRNGELVIEHKGFIYISQTFPRFOEIKENTKNDKQMOV 119  
 DB 160 --LEWEDT-YGVILLSGVYKKGGLVINEGTFYKSKYFRQ-----SCNNPLSHK 210  
 QY 120 IY-KYTSYDPIILMKARSNS-----CWSKDAEYGLYSYOGIPELKNDRIFVSYTN 172  
 DB 211 VYMRNSKYQDVLVMEGKMSYCTTGQMMAR-----SYLGAVNLISADHLIYVNSE 263  
 QY 173 EHLIDMDHEASFFGAP 188  
 DB 264 LSLVNEESQTEFFGLY 279

## RESULT 7

FASTA\_RAT STANDARD; PRT; 278 AA.  
 AC 036940;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1993 (Rel. 38, Last annotation update)  
 DE FAS ANTIGEN LIGAND.  
 GN TNPSF6 OR APTLIG1 OR FASL.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NC NCBL\_Taxid-10116;  
 RN [1];  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94084792; PubMed-7505205;  
 RA Suda T., Takahashi T., Golstein P., Nagata S.;  
 RT "Molecular cloning and expression of the Fas ligand, a novel member  
 of the tumor necrosis factor family.";  
 RL Cell 75:1169-1178(1993).  
 CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT  
 TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN  
 CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.  
 CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF  
 PERIPHERAL TOLERANCE. IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE  
 T CELLS, OR BOTH.  
 CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).  
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED  
 INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL  
 SURFACE.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND  
 THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,  
 KIDNEY AND LUNG.  
 CC -1- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: 003470; AAC52129.1; -  
 CC InterPro: IPR000478; -  
 CC Pfam: PF00229; TNF\_1; 1.  
 CC PROSITE: PS00251; TNF\_1; 1.  
 CC PROSITE: PS50049; TNF\_2; 1.  
 DR

KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.  
 FT DOMAIN 1 77  
 FT TRANSMEM 78 99  
 FT DOMAIN 100 278  
 FT DOMAIN 100 278  
 FT DOMAIN 4 69  
 FT DOMAIN 45 58  
 FT DISULFID 199 230  
 FT CARBOHYD 116 116  
 FT CARBOHYD 247 247  
 FT CARBOHYD 257 257  
 SQ SEQUENCE 278 AA: 31140 MW: 2898E18A862CEAC6 CRC64;  
 Query Match 17.8%; Score 177.5; DB 1; Length 278;  
 Best Local Similarity 27.5%; Pred. No. 2.5e-08;  
 Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

QY 10 ISTVQKQONTISPLVNERGPORVAHITGT-KRSTLTSSPNSKNEKALGRKINSWESSR 68  
 DB 121 VSSFEKQIANPSTPSETKRPRSV-AHLTGPNRSRSLP-----EWEDT- 162  
 QY 69 SGHSFSLNLRNGELVIEHKGFIYISQTFPRFOEIKENTKNDKQMOVYIY-KYTSY 127  
 DB 163 YGTALISGVYKKGGLVINEAGLIFYSKYFRQ-----SCNSQPLSHKYMRFKTP 216  
 QY 128 DPIILMKARS-NSCWSKDAEYGLYSYOGIPELKNDRIFVSYTNHLLIDMDHEASFFG 186  
 DB 217 GDLVLMEEKKLNCTT--GQIMAHSSYLGAVFNLIVADHLIYVINSQSLINFEESKTFPG 274  
 QY 187 AP 188  
 DB 275 LY 276

## RESULT 8

TN14\_HUMAN STANDARD; PRT; 240 AA.  
 ID TN14\_HUMAN  
 AC 043557; 075476;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 14 (HERPESVIRUS ENTRY  
 MEDIATOR-LIGAND) (HVEM-L).  
 GN TNFSF14 OR LIGHT OR HVEML.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NC NCBL\_Taxid-9606;  
 RN [1];  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98122340; PubMed-9462508;  
 RA Mauri D.N., Edner R., Montgomery R.I., Kochev K.D., Cheung T.C.,  
 RA Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,  
 RA Ware C.F.;  
 RT "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are  
 ligands for herpesvirus entry mediator.";  
 RL Immunity 8:21-30(1998).  
 RN [2];  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC TISSUE=Liver;  
 RX MEDLINE=98438532; PubMed-9765287;  
 RA Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J.,  
 RA Tan K.B., Dede K., Spananato J., Silverman C., Hensley P.,  
 RA DiPietro R., Emery J.G., Deen K., Elchman C., Chabot-Fletcher M.,  
 RA Truneh A., Young P.R.;  
 RT "Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for  
 HVEM/TLR2, stimulates proliferation of T cells and inhibits HT29 cell  
 growth.";  
 RL J. Biol. Chem. 273:27548-27556(1998).  
 CC -1- FUNCTION: ACTIVATES NKs, STIMULATES THE PROLIFERATION OF T CELLS,  
 AND INHIBITS GROWTH OF THE ADENOCARCINOMA HT-29. ENGAGES THE  
 RECEPTOR FOR THE LYMPHOTOXIN-ALPHA-BETA HERPOTRIMER BUT DOES NOT  
 FORM COMPLEXES WITH EITHER LT-ALPHA OR LT-BETA. ACTS AS A RECEPTOR

CC FOR HERPES SIMPLEX VIRUS.

CC -1- SUBUNIT: HOMOTRIMER.

CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).

CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BUT ALSO

CC FOUND IN THE BRAIN. WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID

CC TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIDNEY,

CC AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR

CC NONHEMATOPOIETIC TUMOR LINES.

CC -1- INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION.

CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

CC -----

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CC -----

DR EMBL; AF036581; AAC39563.1; -

DR EMBL; AF064090; AAC25169.1; -

DR MIM; 604520; -

DR HSSP; P01375; ARTSV.

DR InterPro: IPR000478; -

DR Pfam; PF00229; TNF\_1.

DR PROSITE; PS00251; TNF\_1; FALSE\_NEG.

DR PROSITE; PS50049; TNF\_2; 1.

KW Cyokline; Cytotoxicin; Transmembrane; Glycoprotein; Signal-anchor.

FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 38 58 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)

FT DCMAIN 59 240 (POTENTIAL).

FT CANBOYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CONFLICT 214 214 E -> K (IN REF. 2).

SQ SEQUENCE 240 AA; 26351 MW; 49D0BP67E1390B39 CMC64;

Query Match 15.3%; Score 152; DB 1; Length 240;

Best Local Similarity 26.3%; Pred. No. 3.2e-06;

Matches 50; Conservative 30; Mismatches 56; Indels 54; Gaps 8;

QY 23 LVRRGPRQV--AAHITTRGRSNTLSSPNSKNEALGRKINSWSSSGHGFSLNHLR 80

DB 83 LIOGRSHVPMADHLITGANSLLTGSGSP-----LLWE-TDLGLAFELGLSYR 129

QY 81 NGELVTHHEKGFYYIYSCYFFRFOEIKENTKNDKQVOY-----IYRYT 124

DB 130 DGLAVYTKAGYIYISK-----YOLGGVGCPLGLASTITHLKYRT 170

QY 125 -SYDPPILIMKSNRNSCWSKDAEYGLV--SIYQGIPELKEKNDRIEVSVTNEHLIDM-DH 180

DB 171 PRYEELELLTSSQSPGCRATSSSRVWMDSPFLGGVHLEAGEEYVVRDLERLYRLDNG 230

QY 181 EASFEGAFV 190

DB 231 TRSYFGAFV 240

RESULT 9

TNF5\_BOVIN STANDARD: PRT; 261 AA.

AC PS1749;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE CD40 LIGAND (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN GP39).

GN TNF5S OR CD40LG OR CD40L.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

CC Bovidae; Bovinae; Bos.

NCBI\_taxid=9913;

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96006582; PubMed=7590981;
RA Mertens B.E.L.C., Muriuki M., Gaidulis L.;
RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
   and tumor necrosis factor alpha.";
RL Immunogenetics 42:430-431(1995).
CC -I FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
CC STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
CC CC
CC -I SUBUNIT: HOMOTRIMER.
CC -I SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -I SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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DR EMBL; Z48469; CAAB8363.1; -.
DR HSSP; P29965; IALY.
DR InterPro; IPR000478; .
DR Pfam; PF00229; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PSS0049; TNF_2; 1.
KW CytoKine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                          (POTENTIAL).
FT DOMAIN 47 261 EXTRACELLULAR (POTENTIAL).
FT DISUFID 178 218 POTENTIAL.
FT CARBOHYD 240 240 N-LINKED (GLCNAC..)(POTENTIAL).
SQ SEQUENCE 261 AA; 29242 MW; 8491EEFB30A787FD CRC64;

Query Match      14.3%; Score 142; DR 1; Length 261;
Best Local Similarity 27.7%; Pred. No. 2.6e-05;
Matches 49; Conservative 33; Mismatches 69; Indels 26; Gaps 8;

OY 13 VQEKQNISPVLYRRGPORVAHAITGTRGRSNLTSPSKNEKAIGRKINSWESSRGSH 72
   |:|::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 104 VKKEKENENEMKGOEP-IAAH-----ISEASKTTSLV-----QH--APRIY 146

OY 73 FLN--LHLANG-ELVIHEKGFFYYISQTYRFPOEIKENTKNCKOMVOYIYKYTSYDP 129
   ||| : | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 147 TLSNNLVLENGKOLAIVKRGGFYIYTQVTCNSRE---TLQAPEFLASLCIKPSGSE 202

OY 130 ILLKMSARNSGMSDAEGLXSYVGGFELKENDRIYVSTNELIDMDHASFPG 186
   :|::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 203 RILLRAANTHSSSKPC-GQGSIHLGVFEQLSGASVEVNWTPDSQVSHGTGYTFSG 257

RESULT 10
TNFA_RABIT STANDARD: PRT: 235 AA.
AC P04924;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHCTIN).
GN TNF OR TNFA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91065534; PubMed=2249779;
```



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RA Shaikhov A.N., Kupriash D.V., Azizov M.M., Jongeneel C.V.,
RA Noshayev S.A.;
RT "Structural analysis of the rabbit TNF locus, containing the genes
RT encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis
RT factor).";
RL Gene 95:215-221(1990).
RN [2]
RN RP SEQUENCE FROM N.A.
RX MEDLINE-86219712; PubMed-3519138;
RA Ito H., Shirai T., Yamamoto S., Akita M., Kawahara S., Todd C.W.,
RA Wallace R.B.;
RT "Molecular cloning and expression in Escherichia coli of the cDNA
RT coding for rabbit tumor necrosis factor.";
RL DNA 5:149-156(1986).
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- PM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC -----
DR EMBL; M12845; AAA31486.1; -
DR EMBL; M12846; AAA31482.1; -
DR EMBL; M60340; AAA31484.1; -
DR PIR; A25451; A25451.
DR PIR; A25454; A25454.
DR PIR; J50727; J50727.
DR HSP; P01375; TNF.
DR InterPro; IPR000478; -
DR InterPro; IPR002959; -
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01234; TNCRSISFCT.
DR PRINTS; PR01235; TNALPHA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50045; TNF_2; 1.
DR Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1
FT TRANS 80
FT TRANSMEM 36
FT DISULFID 148
FT CONFLICT 63
FT SEQUENCE 235 AA; 25816 MW; 610177DDBDZEF871 CRC64;

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QY 20 ISPLVRECGPRVAAHITGTGRGNTL--SSPNSKNEALOKIUS-----WESSRG 70
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 56 IGPQEEEDSPNNL--HLVNPVAQWTLRSASRALSDKPLAHVAVANPVEGQLOLMSORAN 113
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 71 HSPFLSLNHLRNGELVIEHKGFYLYTSQTYFRFQEEIKENTKNDKOMVQYLYKK--TSYDP 129
    : : : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 114 ALLANGMKLTJDNQILVVPADGJLYLTSQVLSGQ-----GCRSYLHLHTVSPRAVSYPNK 168
    : : : : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 130 IILMKSAARNSCWSKDAETG-----LYSTYOGGIEFLKENDRIFYVTNHLIDMDHEAS- 183
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 169 VNLISAIKSPCHRETPPEAEPEMAWYEPYLYGGVQLEKGRDLSTEVNQPEYDLAESGV 228
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 184 FFG 186
    : : | : |
Db 229 YFG 231

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| AC | AD | AE | AF | AG | AH | AI | AJ | AK | AL | AM | AN | AO | AP | AQ | AR | AS | AT | AV | AW | AX | AY | AZ | BA | BB | BC | BD | BE | BF | BG | BH | BI | BJ | BK | BL | BM | BN | BO | BP | BQ | BR | BS | BT | BV | BW | BX | BY | BZ | CA | CB | CC | CD | CE | CF | CG | CH | CI | CJ | CK | CL | CM | CN | CO | CP | CQ | CR | CS | CT | CU | CV | CW | CX | CY | CZ | DA | DB | DC | DD | DE | DF | DG | DH | DI | DJ | DK | DL | DM | DN | DO | DP | DQ | DR | DS | DT | DU | DV | DW | DX | DY | DZ | EA | EB | EC | ED | EE | EF | EG | EH | EI | EJ | EK | EL | EM | EN | EO | EP | EQ | ER | ES | ET | EU | EV | EW | EX | EY | EZ | FA | FB | FC | FD | FE | FF | FG | FH | FI | FJ | FK | FL | FM | FN | FO | FP | FQ | FR | FS | FT | FU | FV | FW | FX | FY | FZ | GA | GB | GC | GD | GE | GF | GG | GH | GI | GJ | GK | GL | GM | GN | GO | GP | GQ | GR | GS | GT | GU | GV | GW | GX | GY | GZ | HA | HB | HC | HD | HE | HF | HG | HH | HI | HJ | HK | HL | HM | HN | HO | HP | HQ | HR | HS | HT | HU | HV | HW | HX | HY | HZ | IA | IB | IC | ID | IE | IF | IG | IH | II | IJ | IK | IL | IM | IN | IO | IP | IQ | IR | IS | IT | IU | IV | IW | IX | IY | IZ | JA | JB | JC | JD | JE | JF | JG | JH | JI | JJ | JK | JL | JM | JN | JO | JP | JQ | JR | JS | JT | JU | JV | JW | JX | JY | JZ | KA | KB | KC | KD | KE | KF | KG | KH | KI | KJ | KK | KL | KM | KN | KO | KP | KQ | KR | KS | KT | KU | KV | KW | KX | KY | KZ | LA | LB | LC | LD | LE | LF | LG | LH | LI | LJ | LK | LL | LM | LN | LO | LP | LQ | LR | LS | LT | LU | LV | LW | LX | LY | LZ | MA | MB | MC | MD | ME | MF | MG | MH | MI | MJ | MK | ML | MM | MN | MO | MP | MQ | MR | MS | MT | MU | MV | MW | MX | MY | MZ | NA | NB | NC | ND | NE | NF | NG | NH | NI | NJ | NK | NL | NM | NO | NP | NQ | NR | NS | NT | NU | NV | NW | NX | NY | NZ | OA | OB | OC | OD | OE | OF | OG | OH | OI | OJ | OK | OL | OM | ON | OO | OP | OQ | OR | OS | OT | OU | OV | OW | OX | OY | OZ | PA | PB | PC | PD | PE | PF | PG | PH | PI | PJ | PK | PL | PM | PN | PO | PP | PQ | PR | PS | PT | PV | PW | PX | PY | PZ | QA | QB | QC | QD | QE | QF | QG | QH | QI | QJ | QK | QL | QM | QN | QO | QP | QQ | QR | QS | QT | QU | QV | QW | QX | QY | QZ | RA | RB | RC | RD | RE | RF | RG | RH | RI | RJ | RK | RL | RM | RN | RO | RP | RQ | RR | RS | RT | RU | RV | RW | RX | RY | RZ | SA | SB | SC | SD | SE | SF | SG | SH | SI | SJ | SK | SL | SM | SN | SO | SP | SQ | SR | SS | ST | SU | SV | SW | SX | SY | SZ | TA | TB | TC | TD | TE | TF | TG | TH | TI | TJ | TK | TL | TM | TN | TO | TP | TQ | TR | TS | TT | TU | TV | TW | TX | TY | TZ | UA | UB | UC | UD | UE | UF | UG | UH | UI | UJ | UK | UL | UM | UN | UO | UP | UQ | UR | US | UT | UU | UV | UW | UX | UY | UZ | VA | VB | VC | VD | VE | VF | VG | VH | VI | VJ | VK | VL | VM | VN | VO | VP | VQ | VR | VS | VT | VU | VV | VX | VY | VZ | WA | WB | WC | WD | WE | WF | WG | WH | WI | WJ | WK | WL | WM | WN | WO | WP | WQ | WR | WS | WT | WU | WV | WW | WX | WY | WZ | XA | XB | XC | XD | XE | XF | XG | XH | XI | XJ | XK | XL | XM | XN | XO | XP | XQ | XR | XS | XT | XU | XV | XW | XX | XY | XZ | YA | YB | YC | YD | YE | YF | YG | YH | YI | YJ | YK | YL | YM | YN | YO | YP | YQ | YR | YS | YT | YU | YV | YW | YX | YZ | ZA | ZB | ZC | ZD | ZE | ZF | ZG | ZH | ZI | ZJ | ZK | ZL | ZM | ZN | ZO | ZP | ZQ | ZR | ZS | ZT | ZU | ZV | ZW | ZX | ZY | ZZ | AA | AB | AC | AD | AE | AF | AG |
|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|
|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|

|                       |        |                    |       |                |
|-----------------------|--------|--------------------|-------|----------------|
| Query Match           | 13.7%; | Score 136.5;       | DB 1; | Length 235;    |
| Best Local Similarity | 23.0%; | Pred. No. 6.7e-05; |       |                |
| Matches               | 42;    | Conservative       | 37;   | Mismatches 81; |
|                       |        |                    |       | Indels 23;     |
|                       |        |                    |       | Gaps 7;        |

|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 13.5%;           | Score 134.5;       | DB 1;      | Length 204; |
| Best Local Similarity | 24.7%;           | Pred. No. 8.3e-05; |            |             |
| Matches 46;           | Conservative 31; | Mismatches 76;     | Indels 33; | Gaps 7      |



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OY 11 STVECKONINSPLYVERPORAIAHTG-----TRRSNTLSPSPNKNEALRKINS 63
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 42 SAAQPAHOH-FPKHAROTLKPAAHLVDDPSTPDSLNRANT-----DRAFLR----- 88
OY 64 WESSNHSGLFSLNLRNGELVHEKGFYIYSQTFPFROEIKENTKNDKOMVOYIKY 123
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 89 -----HGFL-----LSNNSLLVPTSGILYFYVSGVVFSGEGCFPATFTPLPLANEVOLF 137
OY 124 TS-YDPDLLKMSARNCSWSDAETGYLSTYOGGIFELKENDRIFVSTNNEHLIDMDEHA 182
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 138 SSOYPFHVLPLLSAOKSVCPGPGPW-VRSYVGAVFLTLGGDOLSTRHDGPHLLSPSS 196
OY 183 SFGAF 188
    | | | | |
Db 197 VFFGAF 202

RESULT 12
TNFA_CAVPO
ID TNFA_CAVPO STANDARD; PRT: 234 AA.
AC P51435;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavilidae; Cavia.
OX NCBI_Taxid=101141;
RN 11
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN-HARTLEY; TISSUE-Lung;
RA Yuan H.T., Kelly F.J., Bingle C.D.;
RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
RN 121
RP SEQUENCE FROM N.A.
RC STRAIN-DUNKIN-HARTLEY;
RA MEDLINE=97462215; PubMed=9316485;
RA White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
    factor-alpha.";
RL Am. J. Physiol. 273:L524-L530(1997).
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
    WITH A WIDE VARIETY OF FUNCTIONS. IT CAN CAUSE CYTOLYSIS OF
    CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
    CACHEXIA. IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
    OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
    CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
    CONDITIONS.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY)
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
    EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- PMT: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
    PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
    CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
    AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U39839; AAB06492.1; -.
CC EMBL: U77036; AAB19210.1; -.
CC HSSP: P01375; 2TUN.
CC InterPro: IPR000478; -.

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|   |  |
|---|--|
| DR  | InterPro; IPR002959; .   |
| DR  | Pfam; PF001229; TNF_1.   |
| DR  | PRINTS; PR01234; TMEGROSISFCT.   |
| DR  | PROSITE; PRO1235; TNFALPHA.  |
| DR  | PROSITE; PS00251; TNF_1; 1.  |
| KW  | Cytokine; PS50049; TNF_2; 1.   |
| DR  | Cytochrome; Cytochrom; Transmembrane; Glycoprotein; Signal-anchor.       |
| FT  | PROPEP 1 79  |
| FT  | CHAIN 80 234   |
| FT  | TRANSEM 36 56  |
| FT  | DISULFID 147 178   |
| SO  | SEQUENCE 234 AA; 25793 MW; 7272C940393E7E9B CRC64;                       |
|   |  |
| Query Match   | 13.3%; Score 132.5; DB 1; Length 234;                                    |
| Best Local Similarity                                       | 24.6%; Pred. No. 0.00015; DB 1;  |
| Matches 44; Conservative 33; Mismatches 77; Indels 25; Gaps |  |
| QY  | 28 GPORVAHAHTGT--RGRSNTL---SPSNKNEKALGRKINS-----MESSNGSHFL 74            |
| Dd  | :   :    :   :    :   :    :   :    :   :    :   :    :   :    :   :     |
| Dd  | 57 GPQREGEPPSSGPERRPLAQTLTKLSASQNDNDRKVAVHVVANQQAEEELQLMSKANALLA 116     |
| QY  | 75 SNLHLRNCELYIHEHKGFYYTYSQTYFRFGDEIKRNTKDKNOMQOYLTKY-TSYDDPLL 133       |
| Dd  | : : : : :    :   :    :   :    :   :    :   :    :   :    :   :    :   : |
| Dd  | 117 NGMGISDQVLVPSDGLYLITYSQLFEKGQ----GCPSYLLTHPTVSRLAVSPDKYNLL 171       |
| QY  | 134 KSARNSSSKDAEYG-----LYSYOGIGIFELKENRIFVSTENHIDM-DHEASEFG 186          |
| Dd  | : : : : :    :   :    :   :    :   :    :   :    :   :    :   :    :   : |
| Dd  | 172 SATSPCKKEPRBEAEERKPWEPIYLGVGVRQLQGDRLSAENVLPQYLDPADDSQIYFG 230       |
|   |  |
| RESULT 13   |  |
| TNFA_PIG  | TNFA_PIG STANDARD; PRT; 232 AA.  |
| ID  | P23563;  |
| AC  | 01-NOV-1991 (Rel. 20, Created)   |
| DT  | 01-NOV-1991 (Rel. 20, Last sequence update)                              |
| DT  | 13-JUL-1999 (Rel. 38, Last annotation update)                            |
| DE  | TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).                 |
| GN  | TNF OR TNFA.   |
| OS  | Sus scrofa (Pig).  |
| OC  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;        |
| OC  | Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.                |
| OX  | NCBI_Taxid=9623;   |
| RN  | [1]  |
| RN  | SEQUENCE FROM N.A.   |
| RP  | MEDLINE=91016861; Pubmed=2216741;  |
| RX  | Drews R.T., Coffee B.W., Prestwood A.K., McGraw R.A.;                    |
| RA  | "Gene sequence of porcine tumor necrosis factor alpha.";                 |
| RT  | Nucleic Acids Res. 18:5564-5564(1990).                                   |
| RL  | [2]  |
| RN  | SEQUENCE FROM N.A.   |
| RP  | TISSUE=Liver.  |
| RC  | MEDLINE=91340150; Pubmed=1874444;  |
| RX  | Kuhnert P., Wuehrlich C., Peterhans E., Pauli U.;                        |
| RA  | "The porcine tumor necrosis factor-encoding genes: sequence and          |
| RT  | comparative analysis.";  |
| RL  | Gene 102:171-178(1991).  |
| RN  | [3]  |
| RN  | SEQUENCE FROM N.A.   |
| RP  | TISSUE=Macrophage;   |
| RC  | Choi C.S., Molitor T.W., Lin G.F., Murtaugh M.P.;                        |
| RA  | "Complete nucleotide sequence of a cDNA encoding porcine tumor           |
| RT  | necrosis factor-alpha.";   |
| RL  | Anim. Biotechnol. 2:97-105(1991).  |
| RN  | [4]  |
| RN  | SEQUENCE OF 44-232 FROM N.A.   |
| RP  | MEDLINE=90034181; Pubmed=2478420;  |
| RX  | Pauli U., Beutler B., Peterhans E.;                                      |
| RA  | "Porcine tumor necrosis factor alpha: cloning with the polymerase        |
| RT  | chain reaction and determination of the nucleotide sequence.";           |
| RL  | Gene 81:185-191(1989).   |
| CC  | -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE    |

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CC WITH A WIDE VARIETY OF FUNCTIONS; IT CAN CAUSE CYTOLYSIS OF  
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
CC CACHEXIA. IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE  
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
CC CONDITIONS.  
CC -1- SUBUNIT: HOMOTRIMER.  
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
CC EXTRACELLULAR SOLUBLE FORM.  
CC -1- PMW: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
CC PROTEOLYTIC PROCESSING.  
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
CC CANCER AND INFECTIOIN, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
CC AND MALNUTRITION.  
CC -----  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb.sib.ch).  
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CC EMBL; X54001; CAA37949.1; ;  
CC DR EMBL; X54859; CAA38639.1; ;  
CC DR EMBL; X57321; CAA40591.1; ;  
CC DR EMBL; M29079; AAA31128.1; ;  
CC PIR; S12606; S12606;  
CC DR PIR; S17290; S17290.  
CC PIR; S18965; S18965.  
CC HSSP; P01375; ZTNUN.  
CC InterPro; IPRO00478; ;  
CC Dr InterPro; IPR002959; ;  
CC Pfam; PF00229; TNF_1.  
CC PRINTS; PR01234; TNCRSISRCT.  
CC DR PRINTS; PR01235; TNALPHA.  
CC PROSITE; PS00251; TNF_1; 1.  
CC PROSITE; PS50049; TNF_2; 1.  
CC CytoKine; CycloOxlin; Transmembrane; Glycoprotein; signal-anchor.  
FT CHAIN 1 76  
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT DISUFID 144 176 BY SIMILARTY  
SO SEQUENCE 232 AA; 25254 MW; 65B2BF70ZD99C8BE CRC64;
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OS Peromyscus leucopus (White-footed mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10041;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92218012; PubMed=1348497;
RA Crew M.D., Filipowsky M.E.;
RT "Sequence of the tumor necrosis factor/cachectin (TNF) gene from
RL Peromyscus leucopus (family Cricetidae).";
CC Immunogenetics 35:351-353(1992).
CC -I- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -I- SUBUNIT: HOMOTRIMER.
CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -I- PMW: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -I- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILD HEALTH
CC AND MALNUTRITION.
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-slb.ch).
CC -----
DR EMBL; M59233; AAA40596.1; -.
DR HSSP; P01375; 2TUN.
DR InterPro; IPR000478; -.
DR InterPro; IPR002959; -.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNFCROSISCT.
DR PRINTS; PR01235; TNFALPHA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT FT 1 79
FT CHAIN 1 TUMOR NECROSIS FACTOR.
FT TRANSFM 36 235 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFD 148 179 BY SIMILARITY.
FT CARBOHD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 235 AA; 25822 MW; 235A5CF9CF9A624 CRC64;

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Db 228 VFPG 231

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RESULT 15
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ID TNFS_MOUSE
AC P27548;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD40 LIGAND (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN
DE G39).
GN TNFSF5 OR CD40LG OR CD40L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92244364; Pubmed=1374165;
RA Armitage R., Fanslow W., Sato T.A., Clifford K.N., Struckbine L.,
RA Macduff B.M., Anderson D.M., Gimpe J.S.D., Davis-Smith T.,
RA Maliszewski C.R., Clark E.A., Smith C.A., Grabstein K.H., Cosman D.,
RA Spriggs M.K.;
RT "Molecular and biological characterization of a murine ligand for
RT CD40."
RL Nature 357:80-82(1992).
RN [2]
RP SIMILARITY TO THE TNF FAMILY.
RX MEDLINE=92310561; Pubmed=1377364;
RA Farrah T., Smith C.A.;
RT "Emerging cytokine family."
RL Nature 358:26-26(1992).
RN [3]
RP 3D-STRUCTURE MODELING OF 115-260.
RX MEDLINE=93200072; Pubmed=8095800;
RA Peltch M.C., Jongeneel C.V.;
RT "A 3-D model for the CD40 ligand predicts that it is a compact trimer
RT similar to the tumor necrosis factors."
RL Int. Immunol. 5:233-238(1993).
CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
CC STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
CC T-LYMPHOCYTES.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X65453; CAA46448.1; -.
DR PIR; S21738; S21738.
DR PDB; 1CDA; 31-OCT-93.
DR MGD; MGI:88337; Tnfsf5.
DR InterPro; IPR000478; -.
DR Pfam; PF00229; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 47 260 EXTRACELLULAR (POTENTIAL).
FT DISULFID 177 217 POTENTIAL.
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).

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SQ SEQUENCE 260 AA; 29396 MW; 7E0F34F7473668B7 CRC64;

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Query Match 12.9%; Score 128.5; DB 1; Length 260;
Best Local Similarity 25.3%; Pred. No. 0.00037;
Matches 44; Conservative 35; Mismatches 68; Indels 27; Gaps 8;

QY 4 RTSETISTV---OEKOONISPLVRENGPQVAHITGTRGSRNTLSSPSKNEKALGR 59
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 89 RQFEDLVADITLTKNEKEKNSFEKQDGEDPQIAHV-----VSEANSNAASVL- 137
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 KINSMESSRSGHSFLSNL-HLRNG-ELVIHEKGFYIYSQTFPFOEIKENFRNDKQMV 117
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 138 ---QW-AKKGYITMKSNTVMLENGKQLVTKREGLYIYVTVQTFCSNRE---PSSQRFI 189
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 118 QYIKYISYPPDILMKSARNSCKDAEYGLYSIYOGGIFELKENDRIYVSVT 171
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 190 VGLMLKPSIGSERILKKAANTHSSSOICEQ--QSVHLGVFELQAGASVFVNV 241
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Search completed: October 1, 2001, 11:44:41  
 Job time: 112 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 1, 2001, 11:41:44 ; Search time 12.27 Seconds  
(without alignments)  
320.518 Million cell updates/sec

Title: US-09-479-252-1\_COPY\_91\_281

Perfect score: 996

Sequence: 1 MILPTSEETISIVGEKQONI.....NEHLIDMDHEASFGAFILVG 191

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
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| 2          | 996   | 100.0       | 281    | 3     | US-08-584-031-1   |
| 3          | 996   | 100.0       | 281    | 3     | US-08-780-496-1   |
| 4          | 996   | 100.0       | 281    | 4     | US-08-883-086-10  |
| 5          | 996   | 100.0       | 281    | 5     | PCT-US96-10895-2  |
| 6          | 930   | 93.4        | 177    | 4     | US-09-105-343A-7  |
| 7          | 693   | 69.6        | 291    | 1     | US-08-670-354-6   |
| 8          | 693   | 69.6        | 291    | 5     | PCT-US96-10895-6  |
| 9          | 654   | 65.7        | 183    | 4     | US-09-105-343A-8  |
| 10         | 235.5 | 23.6        | 294    | 3     | US-08-996-139-11  |
| 11         | 235.5 | 23.6        | 316    | 4     | US-08-995-659-11  |
| 12         | 235.5 | 23.6        | 316    | 2     | US-08-842-842-7   |
| 13         | 235.5 | 23.6        | 316    | 4     | US-08-969-362-2   |
| 14         | 232.5 | 23.3        | 317    | 3     | US-08-996-139-13  |
| 15         | 232.5 | 23.3        | 317    | 4     | US-08-995-659-13  |
| 16         | 184.5 | 18.5        | 279    | 5     | PCT-US95-00362-5  |
| 17         | 180   | 18.1        | 281    | 3     | US-08-649-100-9   |
| 18         | 180   | 18.1        | 281    | 2     | US-08-810-453-2   |
| 19         | 180   | 18.1        | 281    | 3     | US-08-815-190A-2  |
| 20         | 180   | 18.1        | 281    | 4     | US-09-290-640-25  |
| 21         | 180   | 18.1        | 281    | 5     | US-09-479-524-3   |
| 22         | 180   | 18.1        | 281    | 5     | PCT-US95-00362-2  |
| 23         | 180   | 18.1        | 287    | 3     | US-08-815-190A-16 |
| 24         | 178   | 17.9        | 145    | 3     | US-08-630-172-5   |
| 25         | 178   | 17.9        | 376    | 3     | US-08-751-512-8   |
| 26         | 178   | 17.9        | 378    | 3     | US-08-630-172-21  |
| 27         | 175.5 | 17.6        | 149    | 3     | US-08-584-031-17  |

|    |       |      |     |   |                   |                    |
|----|-------|------|-----|---|-------------------|--------------------|
| 28 | 154   | 15.5 | 240 | 4 | US-08-913-014A-1  | Sequence 1, Appl   |
| 29 | 152.5 | 15.3 | 239 | 4 | US-08-913-014A-2  | Sequence 2, Appl   |
| 30 | 147.5 | 14.8 | 239 | 4 | US-08-913-014A-3  | Sequence 3, Appl   |
| 31 | 130   | 13.1 | 170 | 6 | 5180811-11        | Patent No. 5180811 |
| 32 | 130   | 13.1 | 170 | 6 | 5180811-13        | Patent No. 5180811 |
| 33 | 128.5 | 12.9 | 260 | 2 | US-08-431-095-2   | Sequence 2, Appl   |
| 34 | 127.5 | 12.8 | 171 | 5 | PCT-US93-02475-11 | Sequence 11, Appl  |
| 35 | 127.5 | 12.8 | 260 | 1 | US-08-446-922-6   | Sequence 6, Appl   |
| 36 | 127.5 | 12.8 | 260 | 2 | US-08-249-189-2   | Sequence 2, Appl   |
| 37 | 127.5 | 12.8 | 260 | 2 | US-08-484-624A-2  | Sequence 2, Appl   |
| 38 | 127.5 | 12.8 | 260 | 2 | US-08-477-733B-2  | Sequence 2, Appl   |
| 39 | 127.5 | 12.8 | 260 | 3 | US-09-088-913A-2  | Sequence 2, Appl   |
| 40 | 127.5 | 12.8 | 260 | 5 | PCT-US93-10034-6  | Sequence 6, Appl   |
| 41 | 127.5 | 12.8 | 280 | 2 | US-08-249-189-23  | Sequence 23, Appl  |
| 42 | 127.5 | 12.8 | 280 | 2 | US-08-484-624A-23 | Sequence 23, Appl  |
| 43 | 127.5 | 12.8 | 280 | 2 | US-08-477-733B-23 | Sequence 23, Appl  |
| 44 | 127.5 | 12.8 | 280 | 3 | US-09-088-913A-23 | Sequence 23, Appl  |
| 45 | 125.5 | 12.6 | 161 | 1 | US-07-994-469A-61 | Sequence 61, Appl  |

## ALIGNMENTS

RESULT 1  
US-08-670-354-2  
; Sequence 2, Application US/08670354  
; Patent No. 5763223  
; GENERAL INFORMATION:  
; APPLICANT: Steven R. Wiley and  
; APPLICANT: Raymond G. Goodwin.  
; TITLE OF INVENTION: Cytokine That Induces Apoptosis  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.5.2  
; SOFTWARE: Microsoft Word, Version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/670,354  
; FILING DATE: 25-JUN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/496,632  
; FILING DATE: 29-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/548,368  
; FILING DATE: 01-NOV-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Anderson, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2835-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-670-354-2

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| Matches               | 191:   | Conservative  | 0:   | Mismatches | 0:     | Indels |
|                       |        |   |      |            | 0:     | Gaps   |
| OY                    | 1      | MILRTSEETISTVQEKQONISPLVBERGPQVAAHITGRGSNTLSSPNSKNEKALGRK | 60   |            |        |        |
| Db                    | 91     | MLRFSSEETISIVQCKOONISPLVBERGPQVAAHITGRGSNTLSSPNSKNEKALGRK | 150  |            |        |        |
| OY                    | 61     | INSWSSRSRGSHFLNHLRNGELVIHEHGEFYIYSOTFREROEIKENTKDKQWQYI   | 120  |            |        |        |
| Db                    | 151    | INSWSSRSRGSHFLNHLRNGELVIHEHGEFYIYSOTFREROEIKENTKDKQWQYI   | 210  |            |        |        |
| OY                    | 121    | YKYIYSPPDILMKARSNCWSKDAEYGLYSITYGQIFELKENDRIFVSVTNEHLIDMH | 180  |            |        |        |
| Db                    | 211    | YKYIYSPPDILMKARSNCWSKDAEYGLYSITYGQIFELKENDRIFVSVTNEHLIDMH | 270  |            |        |        |
| OY                    | 181    | EASFEGAFVNG   | 191  |            |        |        |
| Db                    | 271    | EASFEGAFVNG   | 281  |            |        |        |

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US-08-584-031-1
US-08-584-031-1
: Sequence 1, Application US/08584031A
: Patent No. 6030945
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: TITLE OF INVENTION: APO-2 LIGAND
: FILE REFERENCE: 11669.2,20503
: CURRENT APPLICATION NUMBER: US/08/584,031A
: CURRENT FILING DATE: 1996-01-09
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 281
: TYPE: PRT
: ORGANISM: Homo sapiens
US-08-584-031-1

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|    | Matches 191:          | Conservative 0:  | Mismatches 0: | Indels 0: | Gaps 0:     |
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| Db | 91                    | MILRFSSEETISTVQEKQOONISPLVBERGQPVAAHITGTRGSNTLSPDPSNKEKALGRK | 150           |           |             |
| QY | 61                    | INSMSSSSGSHFSLNLRNGELVTHEGFGYIYSQYFPRFOEELKEFTKNDKQOVYI      | 120           |           |             |
| Db | 151                   | INSMSSSSGSHFSLNLRNGELVTHEGFGYIYSQYFPRFOEELKEFTKNDKQOVYI      | 210           |           |             |
| QY | 121                   | YKYTSYPPPIILMKARSARCSCKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDH | 180           |           |             |
| Db | 211                   | YKYTSYPPPIILMKARSARCSCKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDH | 270           |           |             |
| QY | 181                   | EASFPGATLVG 191  |               |           |             |
| Db | 271                   | EASFPGATLVG 281  |               |           |             |

RESULT 3  
US-08-780-496-1  
: Sequence 1, Application US/08780496  
: Patent No. 6046048  
: GENERAL INFORMATION:  
: APPLICANT: AVI Ashkenazi, Anan Chuncharapai, Kyung Jin Kim  
: TITLE OF INVENTION: Apo-2 Ligand  
: NUMBER OF SEQUENCES: 8  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Genentech, Inc.  
: STREET: 460 Point San Bruno Blvd  
: CITY: South San Francisco

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1 STATE: California
2
3 COUNTRY: USA
4
5 ZIP: 94080
6
7 COMPUTER RELEASABLE FORM:
8
9 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
10
11 COMPUTER: IBM PC compatible
12
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14
15 SOFTWARE: Winpatin (Genentech)
16
17 CURRENT APPLICATION DATA:
18
19 APPLICATION NUMBER: US/08/780,496
20
21 FILING DATE: 08-Jan-1997
22
23 CLASSIFICATION: 435
24
25 ATTORNEY/AGENT INFORMATION:
26
27 NAME: Mairschany, Diane L.
28
29 REGISTRATION NUMBER: 35,600
30
31 REFERENCE/DOCKET NUMBER: P0978P1
32
33 TELECOMMUNICATION INFORMATION:
34
35 TELEPHONE: 415/225-5416
36
37 TELEFAX: 415/952-9881
38
39 TELE: 910/371-7168
40
41 INFORMATION FOR SEQ ID NO.: 1:
42
43 SEQUENCE CHARACTERISTICS:
44
45 LENGTH: 281 amino acids
46
47 type: Amino acid
48
49 TOPOLOGY: Linear
50
51 US-08-780-496-1

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|                       |                 |                    |           |             |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match           | 100.0%;         | Score 996;         | DB 3;     | Length 281; |
| Best Local Similarity | 100.0%;         | Pred. No. 3.8e-98; |           |             |
| Matches 191;          | Conservative 0; | Mismatches 0;      | Indels 0; | Gaps 0;     |

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| Db | 91  | MILRSEETISTYVEKÖÖNISPVLAREKQPÖVAHINTGRSRSTLSPMSNKALGR     | 150 |
| Qy | 61  | INSWESSRSGHSFLSNLHRLNGELVHEKGFYYIYSQTYERFOELKENTRNDKÖWÖYI | 120 |
| Db | 151 | INSWESSRSGHSFLSNLHRLNGELVHEKGFYYIYSQTYERFOELKENTRNDKÖWÖYI | 210 |
| Qy | 121 | YKYTSYPPPIILMKSARNSCSKAEBGLSITYGGIFELKENDRIVSYTNEHLDMDH   | 180 |
| Db | 211 | YKYTSYPPPIILMKSARNSCSKAEBGLSITYGGIFELKENDRIVSYTNEHLDMDH   | 270 |
| Qy | 181 | EASFEGAFVIG 191   |     |
| Db | 271 | EASFEGAFVIG 281   |     |

RESULT 4  
US-08-883-086-10  
Sequence 10, Application US/08883086  
Patent No. 6171787  
GENERAL INFORMATION:  
APPLICANT: WILEY, STEVEN  
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL  
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEO Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/883.086  
FILING DATE:

RESULT 5  
PCT-US96-10895-2  
Sequence 2, Application PC/TUS9610895  
GENERAL INFORMATION:  
APPLICANT: Immunex Corporation.  
TITLE OF INVENTION: Cytokine That Induces Apoptosis  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.5.2  
SOFTWARE: Microsoft Word, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10895  
FILING DATE: 25-JUN-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/496,632  
FILING DATE: 29-JUN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/548,368  
FILING DATE: 01-NOV-1995

RESULT. 6  
 ; Sequence 7, Application US/09105343A  
 ; Patent No. 6207642  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WILEY, S. R.  
 ; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL  
 ; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: Abbott Laboratories  
 ; STREET: 100 Abbott Park Road  
 ; CITY: Abbott Park  
 ; STATE: IL  
 ; COUNTRY: USA  
 ; ZIP: 60064-6050  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows  
 ; SOFTWARE: FASSEQ for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/105,343A  
 ; FILING DATE: 12-FEB-1998  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US98/02859  
 ; FILING DATE: 12-FEB-1998  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BECKER, Cheryl L.  
 ; REGISTRATION NUMBER: 35,441  
 ; REFERENCE/DOCKET NUMBER: 6048.US.P2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 847-935-1729



```

; TELEFAX: 847-938-2623
;
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO. 6207642e
; US-09-105-343A-7

Query Match          93.4%; Score 930; DB 4; Length 177;
Best Local Similarity 99.4%; Pred. No. 2.1e-91;
Matches 176; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EKOQNISPLVREKGPORVAHAITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFL 74
DB 1 EKOQNISPLVREKGPORVAHAITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFL 60
QY 75 SNLHNLNGELVYHEKGFYYIYSQTYFRFQEEIKENTKNDKQWQYIYKTYSPDPILMK 134
DB 61 SNLHNLNGELVYHEKGFYYIYSQTYFRFQEEIKENTKNDKQWQYIYKTYSPDPILMK 120
QY 135 SARNSCWSKDAEYGLXSYIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 191
DB 121 SARNSCWSKDAEYGLXSYIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG 177

RESULT 7
US-08-670-354-6
; Sequence 6, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Willey and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670.354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
```

```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-670-354-6

Query Match          69.6%; Score 693; DB 1; Length 291;
Best Local Similarity 69.1%; Pred. No. 6.8e-66;
Matches 134; Conservative 23; Mismatches 31; Indels 6; Gaps 1;

QY 3 LRTSEETISTVOEKOQNISPLVREKGPORVAHAITGTRGRSNTLSSPNSKNEKALGRKIN 62
DB 97 LRTFODTISTVPEKOLSTPLRGRGPQKVAHAITGTRRSNLSALIPISKDKTIGQKIE 156
QY 63 SWESSRSGHSLNLNLNGELVYHEKGFYYIYSQTYFRFQEE-----IKENTKNDKQW 116
DB 157 SWESSRSGHSLNLNLNGELVYHEKGFYYIYSQTYFRFQEEADSKWVSKDKVTKQL 216
QY 117 VOYIYKTYSPDPILMKARNSCWSKDAEYGLXSYIOGGIFELKENDRIFVSVTNEHLI 176
DB 217 VOYIYKTYSPDPILMKARNSCWSKDAEYGLXSYIOGGIFELKENDRIFVSVTNEHLI 276
QY 177 DMDHEASFFGAFIV 190
DB 277 DMDHEASFFGAFIV 290

RESULT 8
PCT-US96-10895-6
; Sequence 6, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-10895-6
```

```

Query Match          69.6%. Score 693; DB 5; Length 291;
Best Local Similarity 69.1%. Pred. No. 6.8e-66;
Matches 134; Conservative 23; Mismatches 31; Indels 6; Gaps 1.

QY      3 LRTSETISTVQEOKQNTISPLVERGPORVAHITGTRGRNSMTLSSPNSKNEKALGRKIN 62
        ||| :||| | | | | | : | | :| | | | | | | | | | | | | | | | | | |
Db      97 LRTFDPTISTVPERKGLSPPLPRGRPOKVAAHIGITRRSASALIPISKDCKTIGOKTE 156
        ||| :||| | | | | | : | | :| | | | | | | | | | | | | | | | | | |

QY      63 SWESSRSCHSFSLNHLNGELVTHEKGFIYYISOTYFRFOE-----IKENTNDKOM 116
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      157 SWESSRKHSHSEFNHLNFGRLGVIEOGLIYYISOTYFRFOEADASKWVSXDKVTKTOL 216
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      117 VOYIKYITSYPPIILMKSARNSCMKAEXGLYSIOGGIRELEKENDRIFFSVNHELI 176
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      217 VOYIKYITSYDPYLMLKSARNSCMSRDEKGYLSITYOGGLELKNDRIFFSVNHELM 276
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      177 DMDHEASEFAGFLV 190
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      277 DLDGEASEFAGFLI 290
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT      9
US-09-105-343A-8
: Sequence 8, Application US/09105343A
: Patent No. 6207642
: GENERAL INFORMATION:
: APPLICANT: WILEY, S.R.
: TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
: TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESSES:
: ADDRESSSEE: Abbott Laboratories
: STREET: 100 Abbott Park Road
: CITY: Abbott Park
: STATE: IL
: COUNTRY: USA
: ZIP: 60064-6050
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows
: SOFTWARE: FastSeq for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/105.343A
: FILING DATE: 12-FEB-1998
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US98/02859
: FILING DATE: 12-FEB-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: BECKER, Cheryl L.
: REGISTRATION NUMBER: 35,441
: REFERENCE/DOCKET NUMBER: 6048 US..P2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 847-935-1729
: TELEFAX: 847-938-2623
: TELEX:
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 183 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: No. 6207642e
US-09-105-343A-8

Query Match          65.7%. Score 654; DB 4; Length 183;
Best Local Similarity 68.7%. Pred. No. 4.9e-62;
Matches 125; Conservative 22; Mismatches 23; Indels 6; Gaps 1.

```

```

QY      15 EKOONISPLVERGRGPOVVAHITGTGSNTJSSPNSKNEMLGKRINSESSRSGHFL 74
       ||| : | | : ||||| ||| : | | : ||||| |||||
Db      1 EQOLSTPPLPGRGCRPKAAAHITGLTRRSNALIPISKOKTILGOKIESWESSRKGHSL 60
       ||| : | | : ||||| ||| : | | : ||||| |||||
QY      75 SNLHLRNGELVLTHENGFYIYSQTYFRFOE-----IKENTKNDKOMVOYIKYTSYPD 128
       :: ||||| :: | ||||| ||||| :: ||||| |||||
Db      61 NHVLRFRNGLVLEIGELYYITSQTYFRFQEAEDASKMWSKDVRTQLVQYIKKYTSYPD 120
       ||| : | | : ||||| ||| : | | : ||||| |||||
QY      129 PILLKKSARNCSWSDAEGLYSIIYGIFELKENDRIVSVTNHEHLIMDHESFFGAF 188
       ||| : | | : ||||| ||| : | | : ||||| |||||
Db      121 PIVLKMSARNSCWSRDAEAGLYSIYOGIFELKKNDRIVSVTNEHLMDLDDEASFFGAF 180
       ||| : | | : ||||| ||| : | | : ||||| |||||
QY      189 LV 190
       :: ::
Db      181 II 182

RESULT 10
US-08-996-139-11
; Sequence 11, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Power Macintosh
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-996-139-11

Query Match          23.6%; Score 235.5; DB 3; Length 294;
Best Local Similarity 29.3%; Pred. No. 3.le-17;
Matches    65; Conservative   37; Mismatches   67; Indels    53; Gaps     7

```

Db SEDTLPDSCRRMKAFQAGVAKELDHVY-----GPGRFSGAPARMEGSLDYAAQGRKPE 138  
 QY 34 ----AHITGTGRBNTLTSSPKNKEKALGKRINSWESSRBSGHTLSMLHRLNGELYIHEK 89  
 Db 139 AQPAAHLT-----INAASTPBGSHKVTL---SSWYHDR-GMAKISMTLSNKLRYNOD 188  
 QY 90 GFVYIYSQTYERFOELKEKNTKNDKNDKQWQYIYKKT-SYPPILIMKSAARNSCMSDAEYG 148  
 Db 189 GFYLLANICRHHETSGSVPTDQLAMTVVVKRSIKPSSHMLMKGGSTKNWNGSEFH 248  
 QY 149 LYSTVGIGFELKENDRIPLFSVTNEHLIMDDHEASFGAGFLV 190  
 Db 249 FYSTINVGFEFLRAGEELSTIYSNPSTLDEPDQDATTYGARKV 290

RESULT 11  
US-08-995-659-11  
; Sequence 11, Application US/08995659

```

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh.
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US59 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US59 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US59 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-995-659-11

```

|                          |        |                    |            |             |
|--------------------------|--------|--------------------|------------|-------------|
| Query Match              | 23.68; | Score 235.5;       | DB 4;      | Length 294; |
| Best Local Similarity    | 29.38; | Pred. No. 3.1e-17; |            |             |
| Matches 65; Conservative | 37;    | Mismatches 67;     | Indels 53; | Gaps 7      |

```

QY 6 SEET-----STVEKOOINSLPREGPOKPA-----33
    |||: |||: |||: |||:
Db 85 SEDTLPBSCRKMAKAFQAVAKELOHY-----GPORFSAAPALMGSLDVAQORKE 138
    |||: |||: |||: |||:
QY 34 ---AHITGTRGASNTLSPNSKNEKALGRKINSMESSRGSCHFSLMLHNGELYIHEK 89
    |||: |||: |||: |||: |||: |||: |||: |||:
Db 139 AQPFALHT-----INAAISIPGSHKVTL-----SSWYHDR-GMAKISNWTLSNGLKLRVNO 188
    |||: |||: |||: |||: |||: |||: |||: |||:
QY 90 GFYYIYISOTYRPFDEIKENKKNOKWQYIYIKT-SYDPDILMKASRNSCKSKDAEYG 148
    |||: |||: |||: |||: |||: |||: |||: |||:
Db 189 GFYYIYAIACIRHNETSGSVPTDLQIMWYVVKISIKIPSSHMLKMGKSTKNSGSEHF 248
    |||: |||: |||: |||: |||: |||: |||: |||:
QY 149 LYSIVGIFELKENDRIJFVSVTNEHLIDMDHKAESPFGAFV 190
    |||: |||: |||: |||: |||: |||: |||: |||:
Db 249 FYSIVGSGFFKLRAGEELISIVSNPSLIDPDODATTYGAFV 290
    |||: |||: |||: |||: |||: |||: |||: |||:

```

## RESULT 12

Sequence 7, Application US/08842842  
Patent No. 5843678  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
TITLE OF INVENTION: OSMOREGULIN BINDING PROTEINS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91330-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/842,842  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-451  
INFORMATION FOR SEQ. ID NO.: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 316 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-842-842-7

|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 23.68;           | Score 235.5;       | DB 2;      | Length 316; |
| Best Local Similarity | 29.38;           | Pred. No. 3.5e-17; |            |             |
| Matches 65;           | Conservative 37; | Mismatches 67;     | Indels 53; | Gaps 7      |

```
OY      6 SEERT-----STVEKOONISPLREBGRPA-----          33
        |||:         |||:         |||:         |||:
DB     107 SEDTLPDSCRMKAFOGAVOKELOHV-----GPFRSGAPAMMGSLUDVAQKPE 160
OY      34 ----AHITGTGRNSNTLSPSNKNEKALGRKINSMESSRGSHFLSMLHNGELYIHEK 89
        |||:         |||:         |||:         |||:         |||:
DB     161 AQPFAHLT-----INAAISIPSGSHKVTL-----SSWYHDR-GMAKISNMTLNCKGLRVNO 210
OY      90 GFYYIYSOTYRROBEIKENTKNDKOWOIYIKTT-SYPPILIMKSARRMSKDAEYG 148
        |||:         |||:         |||:         |||:         |||:
DB     211 GFYYLYANICRHNETSGSVPTDIOLATMVAVKTSIRIPSCHNLMKGGSTKMSGNSEFH 270
OY      149 LYSTOGGFEELKENDRFVATVTEHLLDMHMEFPGAFV 190
        |||:         |||:         |||:         |||:         |||:
DB     271 FYSIVNGGEFKLRAGEETISDVNSPBLDPPODATTYGAEEV 312
```



;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Immunex Corporation, Law Department  
;; STREET: 51 University Street  
;; CITY: Seattle  
;; STATE: WA  
;; COUNTRY: USA  
;; ZIP: 98101  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: Apple Power Macintosh  
;; OPERATING SYSTEM: Apple Operating System 7.5.5  
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/995,659  
;; FILING DATE: 22 DECEMBER 1997  
;;  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: USSN 60/064,671  
;; FILING DATE: 14 OCTOBER 1997  
;;  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: USSN 08/813,509  
;; FILING DATE: 07 MARCH 1997  
;;  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: USSN 08/772,330  
;; FILING DATE: 23 DECEMBER 1996  
;;  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Perkins, Patricia Anne  
;; REGISTRATION NUMBER: 34,693  
;; REFERENCE/DOCKET NUMBER: 2852-A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; INFORMATION FOR SEQ ID NO: 13:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 317 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;;  
;; US-08-995-659-13

Query Match 23.3%; Score 232.5; DB 4; Length 317;  
Best Local Similarity 32.9%; Pred. No. 7.2e-17;  
Matches 52; Conservative 33; Mismatches 62; Indels 11; Gaps 4;  
QY 34 AHITGRGRSNTLSSPSNKKERKALGRKINWESSRSGHSFLSNLHLRNGELVYIHEKGFY 93  
DB 166 AHIT-----INATDIPSGSHKVSLS---SSWYHDR-GWAKISNMTFSNGKLIYNODGFIY 215  
QY 94 IYSQYFRFOEIEIKENWKNDKQWQYIKYT-SYDPILMKSRNSCWKDAEYGLYSI 152  
DB 216 LVANICFRHHTETGDLATELQMLVYVTKSIKIPSSHILMKGSGTKYWSGNSFHFYSI 275  
QY 153 YGGIFELKENDRIEVSVINEHLIDMDHEASFGAFVY 190  
DB 276 NVGGFFKLSGSEISIEVSNPILDPDQATYFGAFKV 313

Search completed: October 1, 2001, 11:43:33  
Job time: 109 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 1, 2001, 11:40:13 ; Search time 20.84 Seconds

(without alignments)  
555.623 Million cell updates/sec

Title: US-09-479-252-1\_COPY\_91\_281

Perfect score: 996  
Sequence: 1 MLPTSEETISTVQEKQONI.....NEHLIDMDHEASFGAFVIG 191

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_0601:\*

- 1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:\*
- 2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:\*
- 3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:\*
- 4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT:\*
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- 9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT:\*
- 10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT:\*
- 11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT:\*
- 12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT:\*
- 13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT:\*
- 14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT:\*
- 15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT:\*
- 16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:\*
- 17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT:\*
- 18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT:\*
- 19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:\*
- 20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:\*
- 21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:\*
- 22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 996   | 100.0       | 279    | 19    | AAW76332    |
| 2          | 996   | 100.0       | 279    | 20    | AAW95032    |
| 3          | 996   | 100.0       | 281    | 18    | AAW27134    |
| 4          | 996   | 100.0       | 281    | 18    | AAW19787    |
| 5          | 996   | 100.0       | 281    | 18    | AAW19777    |
| 6          | 996   | 100.0       | 281    | 19    | AAW6829     |
| 7          | 996   | 100.0       | 281    | 19    | AAW56760    |
| 8          | 996   | 100.0       | 281    | 19    | AAW44354    |
| 9          | 996   | 100.0       | 281    | 20    | AAW27012    |
| 10         | 996   | 100.0       | 281    | 20    | AAW01517    |
| 11         | 996   | 100.0       | 281    | 21    | AAW28691    |

|    |       |       |     |    |          |                     |
|----|-------|-------|-----|----|----------|---------------------|
| 12 | 996   | 100.0 | 281 | 21 | AAW24038 | Human PRO1096 prot  |
| 13 | 996   | 100.0 | 281 | 21 | AAW08545 | Amino acid sequenc  |
| 14 | 996   | 100.0 | 281 | 21 | AAW81956 | Human Apo-2 ligand  |
| 15 | 996   | 100.0 | 281 | 22 | AAW8350  | Human TL2 polypept  |
| 16 | 996   | 100.0 | 281 | 22 | AAW67243 | Human Apo2 ligand.  |
| 17 | 996   | 100.0 | 281 | 22 | AAW50977 | Human PRO1096 prot  |
| 18 | 989   | 99.3  | 281 | 20 | AAW01516 | Protein associated  |
| 19 | 988   | 99.2  | 281 | 20 | AAW27016 | Human Apo-2 ligand  |
| 20 | 988   | 99.2  | 281 | 20 | AAW27017 | Human Apo-2 ligand  |
| 21 | 988   | 99.2  | 281 | 20 | AAW27018 | Human Apo-2 ligand  |
| 22 | 974   | 97.8  | 281 | 21 | AAW28692 | Fc-huApo-1 (95-281  |
| 23 | 972   | 97.6  | 281 | 20 | AAW27019 | Human Apo-2 ligand  |
| 24 | 953.5 | 95.7  | 220 | 21 | AAW86630 | Cell factor deriva  |
| 25 | 893.5 | 89.7  | 423 | 21 | AAW28693 | Fc-huApo-1 (114-28  |
| 26 | 878   | 88.2  | 166 | 21 | AAW08274 | Amino acid sequenc  |
| 27 | 850   | 85.3  | 161 | 22 | AAW71985 | C-terminal region   |
| 28 | 727   | 73.0  | 139 | 20 | AAW01518 | Polypeptide of the  |
| 29 | 693   | 69.6  | 291 | 18 | AAW19788 | Mouse apoptosis in  |
| 30 | 693   | 69.6  | 291 | 19 | AAW56762 | Murine TRAIL polyp  |
| 31 | 693   | 69.6  | 291 | 19 | AAW4353  | Murine AGP-1. Mus   |
| 32 | 686   | 68.9  | 448 | 21 | AAW28694 | Fc-muApo-1 (99-291  |
| 33 | 639.5 | 64.2  | 426 | 21 | AAW28695 | Fc-muApo-1 (120-29  |
| 34 | 633   | 63.6  | 172 | 21 | AAW08275 | Amino acid sequenc  |
| 35 | 235.5 | 23.6  | 244 | 19 | AAW63019 | A murine OCIF-bind  |
| 36 | 235.5 | 23.6  | 294 | 19 | AAW69956 | NF-KB receptor act  |
| 37 | 235.5 | 23.6  | 294 | 19 | AAW68292 | NF-KB receptor act  |
| 38 | 235.5 | 23.6  | 316 | 19 | AAW83194 | Human osteoprotege  |
| 39 | 235.5 | 23.6  | 316 | 19 | AAW83017 | Osteoclastogenesis  |
| 40 | 235.5 | 23.6  | 316 | 19 | AAW59654 | Murine acid sequenc |
| 41 | 235.5 | 23.6  | 316 | 20 | AAW17874 | Murine TRANCE. Mu   |
| 42 | 235.5 | 23.6  | 316 | 21 | AAW91024 | Mouse OBM protein   |
| 43 | 235.5 | 23.6  | 316 | 21 | AAW84418 | Amino acid sequenc  |
| 44 | 235.5 | 23.6  | 316 | 21 | AAW84419 | Amino acid sequenc  |
| 45 | 232.5 | 23.3  | 152 | 22 | AAW67248 | Human RANKL. Homo   |

#### ALIGNMENTS

|          |   |
|----------|---|
| RESULT   | 1   |
| AAW76332 | standard; Protein: 279 AA.  |
| ID       | AAW76332  |
| XX       | AAW76332;   |
| AC       | AAW76332;   |
| XX       |   |
| DT       | 11-JAN-1999 (first entry)   |
| XX       |   |
| DE       | Human TL2 (TRAIL), ligand for TR5.                                |
| XX       |   |
| KW       | TL2; TRAIL; tumor necrosis related receptor; TR5; inflammation;   |
| KW       | arthritis; septicemia; transplant rejection; autoimmune disease;  |
| KW       | inflammatory bowel disease; graft versus host disease; infection; |
| KW       | stroke; ischemia; acute respiratory disease syndrome; psoriasis;  |
| KW       | retinosis; brain injury; AIDS; bone disease; cancer;              |
| KW       | atherosclerosis; Alzheimer's disease; human; therapy; diagnosis;  |
| XX       | ligand.   |
| XX       |   |
| OS       | Homo sapiens.   |
| XX       |   |
| PN       | EP867509-A2.  |
| XX       |   |
| PD       | 30-SEP-1998.  |
| XX       |   |
| PF       | 04-FEB-1998; 98EP-0300827.  |
| XX       |   |
| PR       | 28-JUL-1997; 97US-0901469.  |
| XX       |   |
| PR       | 05-FEB-1997; 97US-0795910.  |
| XX       |   |
| PA       | (SMIK ) SMITHKLINE BEECHAM CORP.                                  |
| XX       |   |
| PI       | Lyn SDP, Tan KB, Truneh A, Young PR;                              |
| XX       |   |
| DR       | WPI; 1998-497862/43.  |

XX New polynucleotide encoding TR5 polypeptide - used to diagnose,  
 PT prevent and treat e.g. inflammation, arthritis, septicemia,  
 PT autoimmune diseases, infections, stroke, ischemia, ARDS, psoriasis,  
 PT restenosis, brain injury, AIDS and bone diseases  
 XX  
 PS Disclosure; Page 17-18; 22pp; English.  
 XX  
 CC This is the amino acid sequence of human TL2 (also known as TRAIL),  
 CC which has newly been discovered to be a ligand of human tumour  
 CC necrosis related receptor TR5 (see AAW76311). This TR5 polypeptide  
 CC of the invention and TL2 can be used in screening processes for  
 CC compounds which bind the receptor, or its ligand, and which  
 CC activate (agonists) or inhibit (antagonists) the receptor or TL2.  
 CC Treatment of a subject with the need to inhibit TR5 polypeptide  
 CC activity comprises administering an antagonist to the polypeptide,  
 CC administering a nucleic acid that inhibits the expression of the  
 CC nucleotide sequence encoding the polypeptide and/or administering a  
 CC polypeptide that competes with the polypeptide for its ligand,  
 CC substrate or receptor. The active agents can be used for the  
 CC treatment of chronic and acute inflammation, arthritis,  
 CC septicemia, autoimmune diseases (e.g. inflammatory bowel disease,  
 CC psoriasis), transplant rejection, graft vs host disease, infection,  
 CC stroke, ischemia, acute respiratory disease syndrome, restenosis,  
 CC brain injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative  
 CC disorders), atherosclerosis and Alzheimer's disease.  
 CC  
 SQ Sequence 279 AA:

Query Match 100.0%; Score 996; DB 19; Length 279;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-94;  
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MIRTSEETSTVOEKOONISPLVRRGPOVAHITGRGSRNTLSPNSKNEKALGRK 60  
 |||||||  
 DB .89 mlrtseetstvgekgqnlspivtergprvaahltgtrgsntlsspsknekalgrk 148  
 OY 61 INSWESSRSGHSLNLHLNCELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWOYI 120  
 |||||||  
 DB 149 inswessrsgshfslnlhlrngelvihekgyfiysqtyfrfgeelkentkndkqmwyl 208  
 OY 121 YKTSYPPDPIILMKKSARNCSKMDAEGYGLSYOGGIFELKENDRIFVSTNHLIDMH 180  
 |||||||  
 DB 209 yktsypdpillmkksarnscwskdaeyglysyggifelkendrifuvtnehlidmdh 268  
 OY 181 EASFGAFLVG 191  
 |||||||  
 DB 269 easfgaflvg 279

RESULT 2  
 AAW95032  
 ID AAW95032 standard; protein; 279 AA.  
 XX  
 AC AAW95032;  
 XX  
 DT 13-MAY-1999 (first entry)  
 XX  
 DE Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.

XX Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis;  
 KW inflammation; septicemia; autoimmune disease; transplant rejection;  
 KW graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;  
 KW acute respiratory disease syndrome; restenosis, bone disease; cancer;  
 KW atherosclerosis; Alzheimer's disease.

OS Unidentified.  
 XX  
 XX EP897114-A2.  
 XX  
 XX PD 17-FEB-1999.  
 XX

PF 04-JUN-1998; 98EP-0304424.  
 XX  
 XX 29-AUG-1997; 97US-0057550.  
 XX 13-AUG-1997; 97US-0055513.  
 PR 26-AUG-1997; 97US-0056980.  
 XX  
 XX (SMR ) SMITHKLINE BEECHAM CORP.  
 XX  
 XX Brigham-burke MR, Young PR;  
 XX  
 DR WPI; 1999-134308/12.

PT Identifying agonists and antagonists to tumour necrosis factor  
 PT receptor (TNF-R) related polypeptides (TR1, TR2, TL2 and TL4) -  
 PT useful for treating stroke, Alzheimer's disease and AIDS  
 XX  
 PS Disclosure; Page 14-15; 18pp; English.

XX The invention relates to identifying agonists or antagonists to tumour  
 CC necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2  
 CC and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a  
 CC candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2  
 CC or TL4 with a candidate compound in the presence of TR1 or TR2; and (b)  
 CC assessing the ability of the candidate compound to compete with TR1 or  
 CC TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful  
 CC for treating diseases caused by imbalance of TL or TR polypeptide levels,  
 CC which cause: chronic and acute inflammation, arthritis, septicemia,  
 CC autoimmune diseases, transplant rejection, graft vs. host disease,  
 CC infection, stroke, ischemia, acute respiratory disease syndrome,  
 CC restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis  
 CC and Alzheimer's disease. The present sequence represents a TNF-R related  
 CC polypeptide TL2.

SQ Sequence 279 AA:

Query Match 100.0%; Score 996; DB 20; Length 279;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-94;  
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MIRTSEETSTVOEKOONISPLVRRGPOVAHITGRGSRNTLSPNSKNEKALGRK 60  
 |||||||  
 DB 89 mlrtseetstvgekgqnlspivtergprvaahltgtrgsntlsspsknekalgrk 148  
 OY 61 INSWESSRSGHSLNLHLNCELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWOYI 120  
 |||||||  
 DB 149 inswessrsgshfslnlhlrngelvihekgyfiysqtyfrfgeelkentkndkqmwyl 208  
 OY 121 YKTSYPPDPIILMKKSARNCSKMDAEGYGLSYOGGIFELKENDRIFVSTNHLIDMH 180  
 |||||||  
 DB 209 yktsypdpillmkksarnscwskdaeyglysyggifelkendrifuvtnehlidmdh 268  
 OY 181 EASFGAFLVG 191  
 |||||||  
 DB 269 easfgaflvg 279

RESULT 3  
 AAW27134  
 ID AAW27134 standard; protein; 281 AA.  
 XX  
 AC AAW27134;  
 XX  
 DT 02-APR-1998 (first entry)  
 XX  
 DE Human Apoptosis inducing molecule-1 (AIM-1).

XX Apoptosis inducing molecule-1; AIM-1; autoimmune disorder;  
 KW tumour necrosis factor ligand superfamily; AIM-1 altered expression;  
 KW neoplasia inhibition; anti-inflammatory agent.  
 XX  
 OS Homo sapiens.  
 XX



PN M09733899-A1.  
 XX 18-SEP-1997.  
 PD  
 XX  
 PF 14-MAR-1996; 96WO-US03773.  
 XX  
 PR 14-MAR-1996; 96WO-US03773.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM:  
 DR WPI: 1997-470807/43.  
 DR N-PSDB: AAT85210.  
 XX  
 PT New isolated apoptosis inducing molecule-I - used to develop  
 PT products for the diagnosis and therapy of e.g. autoimmune diseases,  
 PT tumours, graft versus host disease or inflammation.  
 PS  
 PS Claim 2; Fig 1; 82pp; English.  
 XX  
 CC The present sequence represents a human Apoptosis inducing molecule-I  
 CC (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand  
 CC superfamily. The products can be used in the diagnosis and treatment of  
 CC disorders related to under-expression, over-expression or altered  
 CC expression of AIM-I. AIM-I or agonists can be used for treating  
 CC autoimmune disorders including systemic lupus erythematosus,  
 CC immunoproliferative disease lymphadenopathy (IPL),  
 CC angioimmunoproliferative lymphadenopathy (AIl), rheumatoid arthritis,  
 CC diabetes, and multiple sclerosis, graft versus host disease, to inhibit  
 CC neoplasia such as tumour cell growth, to treat restenosis, to regulate  
 CC haematopoiesis in endothelial cell development, to stimulate peripheral  
 CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be  
 CC used for treating cachexia, cerebral malaria, rheumatoid arthritis  
 CC or osteoporosis, for preventing graft-host rejection, and as  
 CC anti-inflammatory agents, for treating endotoxic shock or to prevent  
 CC activation of HIV.  
 XX  
 SQ Sequence 281 AA:  
 Query Match 100.0%; Score 996; DB 18; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-94;  
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;  
 XX thrombotic microangioplasty; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Location/Qualifiers  
 FT 1..18  
 FT /label= Cytoplasmic\_domain  
 FT 19..38  
 FT Domain  
 FT /label= Transmembrane\_domain  
 FT 39..281  
 FT /label= Extracellular\_domain  
 FT /note= "contains a receptor-binding region"  
 FT 109..111  
 FT Modified-site  
 FT /note= "potential N-glycosylation site"  
 FT 89..90  
 FT /note= "potential KEX2 protease processing site"  
 FT 149..150  
 FT /note= "potential KEX2 protease processing site"  
 FT  
 XX M09701633-A1.  
 XX 16-JAN-1997.  
 PD  
 XX  
 PF 25-JUN-1996; 96WO-US10895.  
 XX  
 PR 01-NOV-1995; 95US-0548368.  
 PR 29-JUN-1995; 95US-0496632.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Goodwin RG, Wiley SR;  
 XX WPI: 1997-118715/11.  
 DR N-PSDB: AAT72847.  
 DR  
 XX  
 PT TRAIL, a novel cytokine, induces apoptosis in cancer and  
 PT virus-infected cells - useful for treating thrombotic  
 PT microangiopathy, cancer and viral infection and for use in assays  
 XX  
 XX Claim 10; Page 43-44; 62pp; English.  
 XX  
 SQ Sequence 281 AA:  
 Query Match 100.0%; Score 996; DB 18; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-94;  
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 271 easfifaflvg 281

## RESULT 5

ID AAM19777 standard; Protein; 281 AA.

AC AAM19777;

DT 22-SEP-1997 (first entry)

DE Novel cytokine Apo-2 ligand.

KW Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..281

FT Protein /note="Claim 4"

FT Protein /note="Claim 3"

FT Protein /note="Claim 2"

FT Protein /note="Claim 1"

FT Region /label="Cytoplasmic-region"

FT Region /label="Transmembrane-region"

FT Region /label="Extracellular-region"

FT Modified-site 109

FT /label="glycosylation"

FT /note="putative N-linked glycosylation site"

FT W09725428-A1.

FT 17-JUL-1997.

FT 08-JAN-1997; 97MO-US00272.

FT 09-JAN-1996; 96US-0584031.

FT (GENENTECH INC.

FT Ashkenazi AJ, Chuntharapai A, Kim KJ;

FT WPI; 1997-372867/34.

FT N-PSDB; AAT72796.

FT Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce

FT apoptosis for the treatment of breast and colon cancer

FT Claim 4; Fig 1a; 72pp; English.

FT A novel cytokine (AAM19777), designated Apo-2 ligand, induces

FT mammalian cell apoptosis. It is believed to be a member of the

FT tumour necrosis factor cytokine family. Its amino acid sequence

FT was deduced from a cDNA clone (AAT72796). Isolated from a human

FT placental cDNA library. Apo-2 ligand polypeptides, esp. those

FT corresponding to amino acids 114-281, 41-281, 15-281 or 1-281 of

FT Apo-2 ligand, can be produced by culturing cells transformed or

FT transfected with a vector contg. Apo-2 ligand nucleic acid. They

FT can be used to induce apoptosis in mammals and to treat

FT pathological conditions such as cancer (esp. breast or colon

FT cancer) or to raise antibodies useful in diagnostic assays.

FT Sequence 281 AA;

FT

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FT

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FT

FT

Best Local Similarity 100.0%; Pred. No. 3.4e-94; Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MILRTSEETISTVOEQOONISPLVREGRPOVAHAHTGTGRCGRNTLSSPSKNEKLGKR 60

Db 91 MILRTSEETISTVQKQGNISPLVREGRPOVAHAHTGTGRCGRNTLSSPSKNEKLGKR 150

QY 61 INSMESRSQSHFSLNHLNGLVIEHKGFFYYISQYFRFOEIKENTKNDKQVOYI 120

Db 151 INSMESRSQSHFSLNHLNGLVIEHKGFFYYISQYFRFOEIKENTKNDKQVOYI 210

QY 121 YKTTSTYDPDPLLMKSARNSCWSDAEGYLSITQGIPELKEKDRIFVSYTNPHLIDMH 180

Db 211 YKTTSTYDPDPLLMKSARNSCWSDAEGYLSITQGIPELKEKDRIFVSYTNPHLIDMH 270

QY 181 EASFPGAFIVG 191

Db 271 easfifaflvg 281

## RESULT 6

ID AAM76829 standard; Protein; 281 AA.

AC AAM76829;

DT 25-JAN-1999 (first entry)

DE Human TL2 protein.

KW TR6; tumour necrosis factor related receptor; human; treatment; stroke;

KW inflammation; arthritis; septicemia; autoimmune disease; restenosis;

KW transplant rejection; infection; ischaemia; brain injury; bone disease;

KW acute respiratory disease syndrome; acquired autoimmune disease syndrome;

KW AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF; TL2.

KW tumour necrosis factor-related apoptosis-inducing ligand.

KW Homo sapiens.

OS Homo sapiens.

PN EP870827-A2.

XX 14-OCT-1998.

PD 23-DEC-1997; 97EP-0310562.

PF 22-AUG-1997; 97US-0916625.

PR 14-MAR-1997; 97US-0041230.

PR 09-MAY-1997; 97US-0853684.

XX (SMK ) SMITHKLINE BEECHAM CORP.

PA Deen KC, Young PR;

PI WPI; 1998-523156/45.

PI N-PSDB; AAV63096.

DR DNA encoding tumour necrosis factor receptor TR6 - and corresponding

DR polypeptide, antibody, agonist, antagonist, etc

DR disclosure; Page 32-33; 34pp; English.

PS This sequence represents the human tumour necrosis factor (TNF)-related

PS receptor, TL2 (also known as tumour necrosis factor-related

PS apoptosis-inducing ligand, TRAIL). This protein is used in a method

PS resulting in the isolation of the novel human TNF related receptor, TR6.

PS TR6 polypeptides and polynucleotides can be used in the treatment of

PS chronic and acute inflammation, arthritis, septicemia, autoimmune

PS diseases (e.g. inflammatory bowel disease, psoriasis), transplant

PS rejection, graft vs. host disease, infection, stroke, ischaemia, acute

PS respiratory disease syndrome, restenosis, brain injury, (acquired

PS autoimmune disease syndrome) AIDS, bone diseases, cancer (e.g.

PS lympho-proliferative disorders), atherosclerosis and Alzheimers disease.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

SO Sequence 281 AA;

Query Match 100.0%; Score 996; DB 19; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-94;  
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MILRTSEETSTVOEKQONISPLVREGRQVVAHITGRSRNTLSSPNKNEKALGRK 60  
 |||  
 DB 91 mlttseeeltstvyekqgnsplyrerpqgvaahltqtrgrntlsspsnknekalgrk 150  
 |||

OY 61 INSWESSRSGHSFSLNHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQMYI 120  
 |||  
 DB 151 inswessrsghsfslnhlrngelvinekgfyyisqtyfrfgeekentkndkqmyyi 210  
 |||

OY 121 YKRTSYDPDPLILMKARSNCMSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDH 180  
 |||  
 DB 211 ykrtsydpdplllmksarncswskaeayglysiy9g9gfelkendriffsvenehlidmdh 270  
 |||

OY 181 EASFECAFLVG 191  
 |||  
 DB 271 easffgaflvg 281

RESULT 7  
 AAM56760  
 ID AAM56760 standard; Protein: 281 AA.  
 XX  
 AC AAM56760;  
 XX  
 DT 05-AUG-1998 (first entry)  
 XX  
 DE Human TRAIL polypeptide.  
 XX  
 KW Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;  
 XX cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..18  
 FT /note= "N-terminal cytoplasmic domain"  
 FT Region 19..38  
 FT /note= "transmembrane region"  
 FT Domain 39..281  
 FT /note= "extracellular domain"  
 XX  
 PN US5763223-A.  
 XX  
 PD 09-JUN-1998.  
 XX  
 PF 25-JUN-1996; 96US-0670354.  
 XX  
 PR 25-JUN-1996; 96US-0670354.  
 PR 29-JUN-1995; 95US-0496632.  
 PR 01-NOV-1995; 95US-0548368.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Goodwin RG, Willey SR;  
 XX  
 DR WPI: 1998-347332/30.  
 DR N-PSDB; AAV29518.  
 XX  
 PT DNA encoding cytokine TNF-related apoptosis ligand polypeptides -  
 XX useful for producing recombinant polypeptides for research and  
 XX therapy of leukaemia, lymphoma, melanoma and viral infections  
 PS Claim 1; Columns 33-36; 28pp; English.  
 CC This represents a human tumour necrosis factor related apoptosis ligand  
 CC (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce  
 CC apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful

CC for producing the recombinant TRAIL polypeptides, which may be useful in  
 CC studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells  
 CC (e.g. to isolate antigens for vaccine development). The polypeptides can  
 CC be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal  
 CC treatment of blood or bone-marrow), or to treat viral infections.  
 CC  
 SO Sequence 281 AA;

Query Match 100.0%; Score 996; DB 19; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-94;  
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MILRTSEETSTVOEKQONISPLVREGRQVVAHITGRSRNTLSSPNKNEKALGRK 60  
 |||  
 DB 91 mlttseeeltstvyekqgnsplyrerpqgvaahltqtrgrntlsspsnknekalgrk 150  
 |||

OY 61 INSWESSRSGHSFSLNHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQMYI 120  
 |||  
 DB 151 inswessrsghsfslnhlrngelvinekgfyyisqtyfrfgeekentkndkqmyyi 210  
 |||

OY 121 YKRTSYDPDPLILMKARSNCMSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDH 180  
 |||  
 DB 211 ykrtsydpdplllmksarncswskaeayglysiy9g9gfelkendriffsvenehlidmdh 270  
 |||

OY 181 EASFECAFLVG 191  
 |||  
 DB 271 easffgaflvg 281

RESULT 8  
 AAM44354  
 ID AAM44354 standard; Protein: 281 AA.  
 XX  
 AC AAM44354;  
 XX  
 DT 28-MAY-1998 (first entry)  
 XX  
 DE Human AGP-1.  
 XX  
 KW Human; AGP-1; tumour necrosis factor-related protein; TNF;  
 XX inflammation; bone resorption; haematopoietic disease.  
 OS Homo sapiens.  
 XX  
 PN WO9746686-A2.  
 XX  
 PD 11-DEC-1997.  
 XX  
 PF 06-JUN-1997; 97WO-US09895.  
 XX  
 PR 07-JUN-1996; 96US-0660562.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Danilenko DM, Johnson MJ, Simonet WS;  
 XX  
 DR WPI: 1998-042194/04.  
 DR N-PSDB; AAV15295.  
 XX  
 PT Nucleic acid encoding AGP-1, a tumour necrosis factor-related  
 XX protein - useful for creating inflammation, bone resorption and  
 XX haematopoietic diseases  
 PS Claim 7; Page 36-37; 54pp; English.  
 CC The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis  
 CC factor (TNF)-related protein, involved in inflammation, myelopoiesis  
 CC and bone resorption. It has the same nucleic acid and amino acid (aa)  
 CC sequences as the TNF-related apoptosis-induced ligand (TRAIL) described  
 CC in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay  
 CC reagents for detecting AGP-1 expression. Nucleic acid complementary to  
 CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds





|    |                                      |
|----|--------------------------------------|
| PT | polypeptide activity or expression - |
| XX |                                      |
| PS | Claim 61; Fig 36; 226pp; English.    |

CC The present invention describes an antibody that binds to a human  
CC protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780;  
CC PRO3444; PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO3444; PRO3454;  
CC PRO4337; PRO1553; PRO1096; PRO2038; and PRO2262. (I) has  
CC anticancer activity and can be used to diagnose tumours in mammals, by  
CC detecting complex formation when the antibody is contacted with test  
CC cells. Increased expression of genes encoding (I) can also be detected  
CC to diagnose tumours. Agents which inhibit the activity of (I),  
CC especially the antibodies, or an antisense oligonucleotide which  
CC hybridises to genes encoding (I), can be used to inhibit tumour growth,  
CC preferably by inducing cell death. Methods from the present invention  
CC can be used to identify compounds which inhibit the biological activity  
CC of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation  
CC probes used in examples from the present invention for human PRO  
CC sequences. AAC58103 to AAC58122 and AAB24021 to AAB24060 represent human  
CC PRO polynucleotide and protein sequences given in the exemplification of  
CC the present invention.

50 Sequence 281 AA;

|                           |        |                    |       |             |
|---------------------------|--------|--------------------|-------|-------------|
| Query Match               | 100.0% | Score 996;         | DB 21 | Length 281; |
| Best Local Similarity     | 100.0% | Pred. NO. 3.4e-94; |       |             |
| Matches 191; Conservative | 0;     | Mismatches         | 0;    | Gaps 0      |

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | MILPTESEITVQEKONINSPVLREKGPORVAHINTGSRSTUSPSPSKNEKALGR           | 60  |
| Db | 91  | mltteeetstvevkeqgnslpvtrevetpqrvaanltgrtrsnltsspnsknekalgr       | 150 |
| QY | 61  | INSWESSNKGHSFSLNHLRNGELVINEHKGFFYYISQTYERFOEIKENKRNKOMQYI        | 120 |
| Db | 151 | inswesatsgnsflsnhlrngelvtvhekgyfyyisqtyfrfgeektenkndkgmqyI       | 210 |
| QY | 121 | YKTYSTYDPPIILMKSARNCSCKOAEYGLYSIYOGIFELKENDRIFVSTNEHLDMDH        | 180 |
| Db | 211 | yktystypdpilmlksarnscswskaeayglisyysqgyfelfekendrlfvsytnehlldmdh | 270 |
| QY | 181 | EASFEFGALIV 191  |     |
| Db | 271 | eastfifgaltvg 281  |     |

## RESULT 13

AAB08545 standard; Protein; 281 AA.

AC AAB08545;

DT 20-DEC-2000 (first entry)

DE Amino acid sequence of a human TRAIL polypeptide.

KM Human; iRIL; tumour necrosis factor; TNF interleukin-1 receptor type I; IL-1R1; TNF related apoptosis-inducing ligand; tumour cell;  
KM TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;  
KM non-small cell lung carcinoma.

OS Homo sapiens.

PN WO200048619-A1.

PD 24-AUG-2000.

PF 15-FEB-2000; 2000WO-US03891

PR 16-FEB-1999; 99US-0120313.

PA (STRD ) UNIV LEIAND STANFORD JUNIOR.

|    |                      |
|----|----------------------|
| PI | Rosen GD;            |
| XX |                      |
| DR | WPI; 2000-558253/51. |
| DR | N-PSDB; AAA64325.    |

PT Killing of tumour cells, e.g. solid tumours or carcinoma, comprises  
PT administration of synergistic combination of diterpenoid diepoxide and  
PT tumour necrosis factor related apoptosis-inducing ligand -  
XX  
PS Disclosure; Page 23-24; 29pp; English.

Disclosure; Page 23-24; 29pp; English.

CC The present sequence represents a human TRAIL (tumour necrosis factor  
CC (TNF) related apoptosis-inducing ligand) polypeptide. The specification  
CC describes a method for enhanced killing of tumour cells. The method  
CC comprises contacting a susceptible tumour cell with a synergistic mixture  
CC of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined  
CC dosage to kill at least 50 % of the cells. This mixture is synergistic,  
CC and so is active at lower doses and against otherwise resistant cell  
CC lines. The method is used for killing tumour cells, especially solid  
CC tumours or carcinomas (especially mammary carcinoma or non-small cell  
CC lung carcinoma).

SQ Sequence 281 AA;

|                       |                |                   |          |            |
|-----------------------|----------------|-------------------|----------|------------|
| Query Match           | 100.0%         | Score 996         | DB 21    | Length 281 |
| Best Local Similarity | 100.0%         | Pred. No. 3.4e-94 |          |            |
| Matches 191           | Conservative 0 | Mismatches 0      | Indels 0 | Gaps 0     |

[illegible]

## RESULT 14

AAy81956  
ID AAY81956 standard; Protein; 281 AA.

AC AAY81956;

DT 10-JUL-2000 (first entry)

Human Apo-2 ligand protein sequence.

KW Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;  
KW therapy; apoptosis; cancer.

05 Homo sapiens.

PN US6046048-A.

PD 04-APR-2000.

PF 08-JAN-1997; 97US-0780496.

PR 09-JAN-1996; 96US-0009755.

PA (GETH ) GENENTECH INC.

PI Kim KJ, Ashkenazi AJ, Chuntharapai A;

DR MPI: 2000-282690/24.  
DR N-PSDB: AAA07425.  
XX  
PT New isolated monoclonal antibodies having antigen specificity for Apo-2  
PT ligand, e.g. 266, 281 or 5C2, useful for detecting the expression of  
PT Apo-2 ligand serum, and for treating diseases associated with increased  
PT apoptosis -  
XX  
PS Claim 9; Fig 1a; 46pp; English.  
XX  
CC This sequence is the human Apo-2 ligand protein, which is recognised  
CC by monoclonal antibodies produced by the hybridoma cell lines of the  
CC invention. The hybridoma cell lines are deposited under the American Type  
CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258  
CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic  
CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,  
CC tissues, or serum. The antibodies may also be employed as therapeutics.  
CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand  
CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat  
CC pathological conditions or diseases associated with increased  
CC apoptosis. They are also useful for the affinity purification of Apo-2  
CC ligand from recombinant cell culture or natural sources. The Apo-2  
CC ligand itself may be used to treat diseases e.g. cancer, by inducing  
CC apoptosis in cells.  
CC  
XX  
SQ Sequence 281 AA:  
  
Query Match 100.0%; Score 96; DB 21; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.4e-94;  
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MILRTSETSTVOEKQONISPLVREGRPOVAAHITGTRGRSNTLSPNSKNEKALGRK 60  
DB 91 mlrtseeltstvyekqgnspivrerqpvaahtlgtgrsntlsspsnkeakalgrk 150  
QY 61 INSWESSRSGHSFLSNLHNLNGELVIEHEKGFYIYSOTYRFFOEIKENTKNDKQMYI 120  
DB 151 inswessrsghsfslsnhlngelvhiekgfyiysqtyrffgeelkentkndqmyi 210  
QY 121 YKYSYDPDPIILKMSARNSCSKDAEYGLYSIYGQIFELKENDRIFVSVTNEHLIDMDH 180  
DB 211 ykysypdpillmksarnscskdaeyglysiyggifelkendrifsvtnehlmdh 270  
QY 181 EASFGAFIVG 191  
DB 271 easfgafivg 281  
  
RESULT 15  
AAB48350  
ID AAB48350 standard; Protein; 281 AA.  
XX  
AC AAB48350;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Human TL2 polypeptide.  
XX  
KW Tumour necrosis factor; TNF; TNF related receptor; TR6; human; TL2;  
KW antiinflammatory; immunosuppressive; cerebroprotective; vasotropic;  
KW antisthmatic; anti-HIV; osteopathic; cytostatic; antithrombotic;  
KW neurotropic; neuroprotective; antiarthritic; antineumatic; antischismic;  
KW gene therapy; vaccine; TNF-alpha; bone disease; cancer; TRAIL.  
OS Homo sapiens.  
XX  
PN MO200077191-A1.  
XX  
PD 21-DEC-2000.  
XX  
PF 12-JUN-2000; 2000MO-US16134.  
XX

PR 15-JUN-1999; 9905-0333593.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PT Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;  
PT MPI: 2001-112223/12.  
DR N-PSDB: AAC84745.  
XX  
XX  
PT New tumor necrosis factor related receptor TR6 polynucleotides and  
PT polypeptides useful for e.g. for treating chronic and acute  
PT inflammation, arthritis, septicemia, autoimmune diseases, infection,  
PT cancer, bone diseases -  
XX  
PS Disclosure; Page 26; 47pp; English.  
XX  
CC The invention relates to a human tumour necrosis factor (TNF) related  
CC receptor, TR6. TR6 can be expressed by standard recombinant methodology.  
CC The TR6 polypeptides are useful for treating chronic and acute  
CC inflammation, rheumatoid arthritis, septicemia, autoimmune diseases  
CC (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft  
CC vs. host disease, infection, stroke, ischemia, acute respiratory disease  
CC syndrome, asthma, restenosis, brain injury, AIDS, bone diseases, cancer,  
CC atherosclerosis, and Alzheimer's disease. These may also be used to  
CC inhibit production of TNF-alpha and eicosanoids, as research reagents and  
CC materials for discovering treatments and diagnostics to animal and human  
CC diseases. The polypeptides may further be used as immunogens to produce  
CC antibodies immunospecific for the TR6 polypeptides. The polynucleotides  
CC may also be used as hybridization probes for cDNA and genomic DNA, for  
CC isolating full-length cDNAs and genomic clones encoding TR6 and of other  
CC genes having high sequence similarity to TR6 gene, and for chromosome  
CC identification. The present sequence represents a human TL2 polypeptide.  
CC TL2 is also known as TRAIL (TNF-related apoptosis-inducing ligand) and is  
CC a ligand for the TL2 polypeptide.  
XX  
SQ Sequence 281 AA:  
  
Query Match 100.0%; Score 96; DB 22; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.4e-94;  
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MILRTSETSTVOEKQONISPLVREGRPOVAAHITGTRGRSNTLSPNSKNEKALGRK 60  
DB 91 mlrtseeltstvyekqgnspivrerqpvaahtlgtgrsntlsspsnkeakalgrk 150  
QY 61 INSWESSRSGHSFLSNLHNLNGELVIEHEKGFYIYSOTYRFFOEIKENTKNDKQMYI 120  
DB 151 inswessrsghsfslsnhlngelvhiekgfyiysqtyrffgeelkentkndqmyi 210  
QY 121 YKYSYDPDPIILKMSARNSCSKDAEYGLYSIYGQIFELKENDRIFVSVTNEHLIDMDH 180  
DB 211 ykysypdpillmksarnscskdaeyglysiyggifelkendrifsvtnehlmdh 270  
QY 181 EASFGAFIVG 191  
DB 271 easfgafivg 281  
  
Search completed: October 1, 2001, 11:43:14  
Job time: 181 sec



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ID 09R1Y0 PRELIMINARY: PRT: 313 AA.
AC 09R1Y0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE OSTEOCLAST DIFFERENTIATION FACTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=99214075; PubMed=10196481;
RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
RA Ueda M., Higashio K.;
RT "Cloning and characterization of the gene encoding mouse osteoclast
RT differentiation factor."
RL Gene 230:121-127(1999).
DR EMBL; AB022039; BAA36970.1; -.
DR EMBL; AB022036; BAA36970.1; JOINED.
DR EMBL; AB022037; BAA36970.1; JOINED.
DR EMBL; AB022038; BAA36970.1; JOINED.
DR InterPro: IPR000478; 1.
DR Pfam: PF00229; TNF_1.
DR PROSITE: PS50049; TNF_2; 1.
DR SMART: SM00207; TNF; 1.
SQ SEQUENCE 313 AA; 34719 MW; 37D5308BFC2842E CRC64;

Query Match 24.7%; Score 246; DB 11; Length 313;
Best Local Similarity 30.8%; Pred. No. 3.7e-14;
Matches 66; Conservative 39; Mismatches 69; Indels 40; Gaps 7;

OY 6 SEETI-----STVOEKQONISPLVREGRQVAAHTGT-----RGRS---- 43
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
DB 107 SEETLPDSCRMQAQOGAVQKELQHTV-----GQORSAMMGSLDVAQKPKPAQP 160
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
OY 44 -----NTLSSPNSKNEKALGRKINSWESSRSGHSFLNLRLNGELVIEHKGFFYIYSQ 97
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
DB 161 FAHITINAAISIPSGSHKVTL-----SSWYHDR-GWAKISNMTLSNGKLRYVQDGFYYLYAN 215
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
OY 98 TYRPFQEIENKNDKQOMQYIYKT-STPDPILLKMSARNSCWSKDAEYGLXSYQGG 156
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
DB 216 ICRHHEHTSGSVPTDYQLQIMVYVYKTSIKIPSSHNLKMGSTKNWGSSEFHYISINVG 275
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
OY 157 IFELKENDRIEVSVTNEHLIDMDHEASFGAFV 190
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
DB 276 FFKLAGEEISIOVSNPSLDDPDADATYFGAFKV 309
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|

RESULT 3
O9JUK9 PRELIMINARY: PRT: 287 AA.
AC 09JUK9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KB LIGAND 2.
GN RANKL 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ikeda T.;
RT "Receptor activator of NF-kB ligand 2."
RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DL EMBL; AB032771; BAA97257.1; -.
DR InterPro: IPR000478; -.
DR Pfam: PF00229; TNF; 1.
DR PROSITE: PS50049; TNF_2; 1.
SQ SEQUENCE 313 AA; 34719 MW; 37D5308BFC2842E CRC64;

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SQ SEQUENCE 287 AA; 32234 MW; 8B2CE8B4C7B534CC CRC64;

Query Match 23.6%; Score 235.5; DB 11; Length 287;
Best Local Similarity 29.3%; Pred. No. 2.8e-13;
Matches 65; Conservative 37; Mismatches 67; Indels 53; Gaps 7;

OY 6 SEETI-----STVOEKQONISPLVREGRQVAAHTGT-----RGRS---- 33
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
DB 78 SEETLPDSCRMQAQOGAVQKELQHTV-----GQORSAMMGSLDVAQKPKPAQP 131
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
OY 34 ----AHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLRLNGELVIEHKG 89
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
DB 132 AQPFAHIT-----INAAISIPSGSHKVTL-----SSWYHDR-GWAKISNMTLSNGKLRYVQD 181
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
OY 90 GFYYIYSQTFRQPELKEKNTKNDKQOMQYIYKT-STPDPILLKMSARNSCWSKDAEYGL 148
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
DB 182 GFYYLYANICFRHETSGSVPTDYQLQIMVYVYKTSIKIPSSHNLKMGSTKNWGSSEFHY 241
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
OY 149 IYSYQGGIFELKENDRIEVSVTNEHLIDMDHEASFGAFV 190
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
DB 242 FYISINVGFFKLAGEEISIOVSNPSLDDPDADATYFGAFKV 283
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|

RESULT 4
O9JUK8 PRELIMINARY: PRT: 199 AA.
AC 09JUK8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KB LIGAND 3.
GN RANKL 3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ikeda T., Takahashi H., Hirokawa K.;
RT "Somatostatin, a new marker of osteoblast, regulates the expression of
RT RANKL isoforms."
RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DL EMBL; AB032772; BAA97258.1; -.
DR InterPro: IPR000478; -.
DR InterPro: IPR003263; -.
DR Pfam: PF00229; TNF; 1.
DR ProDom: PD008600; -.
DR PROSITE: PS50049; TNF_2; 1.
DR PROSITE: PS50049; TNF_2; 1.
SQ SEQUENCE 199 AA; 22150 MW; 401C13EB5E8CE166 CRC64;

Query Match 23.4%; Score 233.5; DB 11; Length 199;
Best Local Similarity 30.5%; Pred. No. 2.7e-13;
Matches 62; Conservative 35; Mismatches 65; Indels 41; Gaps 6;

OY 13 VOEKQONISPLVREGRQVAAHTGT-----RGRS---- 48
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
DB 9 VQKELQHTV-----GQORSAMMGSLDVAQKPKPAQPFAHIT-----INAAIS 57
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
OY 49 PNSKNEKALGRKINSWESSRSGHSFLNLRLNGELVIEHKGFFYIYSQTFRQPELKE 108
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
DB 58 PSQSHKVTL-----SSWYHDR-GWAKISNMTLSNGKLRYVQDGFYYLYANICFRHETSGS 112
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
OY 109 NTKNDKQOMQYIYKT-STPDPILLKMSARNSCWSKDAEYGLXSYQGGIFELKENDRIE 167
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
DB 113 VPTDYQLQIMVYVYKTSIKIPSSHNLKMGSTKNWGSSEFHYISINVGFFKLAGEEIS 172
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
OY 168 VSYTNEHLIDMDHEASFGAFV 190
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
DB 173 IOVSNPSLDDPDADATYFGAFKV 195
   ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|

```

| Query Match  | Best Local Similarity                  | Matches | 64; Conservative | 35; Mismatches | 68; Indels | 31; Gaps |
|--|--|---------|------------------|----------------|------------|----------|
| 13 VOEKQONISPLVREKGPOR--VAAHITGT-----RGRS-----NTLSSPSNKN 53              | 23.3%; Score 232.5; DB 11; Length 318; |         |                  |                |            |          |
| 128 VORELQHHV-----GPOFSGVPPMMESGSLVDVARRGKPEKOPRAHLTINADIPSGSH 181       | 32.3%; Pred. No. 5.9e-13;              |         |                  |                |            |          |
| 54 EKALGRKINSWESSRSGSFLSLHLRNGELVTHKGFYIYSQTYFRFOEIKENTKND 113           |  |         |                  |                |            |          |
| 182 KYSL-----SWWHDR-GNAKISNMTLSNCKLRVNDGFFYLXLANICFRHHETSGSVADY 236      |  |         |                  |                |            |          |
| 114 KOMVOYITKYT- SYDPTILMKASRNCSDKADEGLYSIYGGIPELKEKNDRIFVSVTN 172       |  |         |                  |                |            |          |
| 237 LQLMYVVKTSIKIPSSNLMKSGSTKMWGSEFHFYSINVGFFKTLRAGEEISVOVSN 296         |  |         |                  |                |            |          |
| 173 EHLIDMDEASPEFGAFV 190  |  |         |                  |                |            |          |
| 297 PSLDPPDODATYEGAFV 314  |  |         |                  |                |            |          |
| RESULT 6   |  |         |                  |                |            |          |
| 09MYL6   | PRELIMINARY:                           | PRT:    | 280 AA.          |                |            |          |
| AC 09MYL6:   |  |         |                  |                |            |          |
| DT 01-OCT-2000 (Tremblrel. 15, Created)                                  |  |         |                  |                |            |          |
| DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)                     |  |         |                  |                |            |          |
| DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)                   |  |         |                  |                |            |          |
| DE RECEPTOR ACTIVATOR OF NF-KB LIGAND.                                   |  |         |                  |                |            |          |
| OS Rattus norvegicus (Rat).  |  |         |                  |                |            |          |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |  |         |                  |                |            |          |
| OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. |  |         |                  |                |            |          |
| NCBI_TaxID=10116;  |  |         |                  |                |            |          |
| SEQUENCE FROM N.A.   |  |         |                  |                |            |          |
| Published=1092398;   |  |         |                  |                |            |          |
| Xu J.K., Tan J., Huang L., Gao X.H., Laird R., Liu D., Wyszocki S.,      |  |         |                  |                |            |          |
| Zheng M.H.;  |  |         |                  |                |            |          |
| "Cloning, sequence and functional characterization of the rat            |  |         |                  |                |            |          |
| homologue of receptor activator of NF-kB ligand."                        |  |         |                  |                |            |          |
| J. Bone Miner. Res. 15:2178-2186(2000).                                  |  |         |                  |                |            |          |
| EMBL; AF187319; AAG17031.1.  |  |         |                  |                |            |          |
| SEQUENCE 318 AA; 35370 MW; 4B87AD706AD098 CRC64;                         |  |         |                  |                |            |          |

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RP      [13]
SEQUENCE FROM N.A. STRAIN-RHESUS MONKEY;
RC SPECIES=M.mullatta;
RA Kirii Y., Inoue T., Yoshino K.;
RT "Rhesus monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035140; BAA90296.1; -
DR EMBL; AB035138; BAA90294.1; -
DR EMBL; AB035138; BAA90295.1; -
DR InterPro; IPR000478; -.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PS01234; TNCRSISFCT.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;

Query Match 18.4%; Score 183; DB 6; Length 280;
Best Local Similarity 27.0%; Pred. No. 1.3e-08;
Matches 50; Conservative 38; Mismatches 73; Indels 24; Gaps 6;

OY 5 TSEETISTYQEQKQINISPLVERGEPORVAAHITGTRGSRNTLSPNSKNEKALGRKINSW 64
DB 117 TTSQKTHASSLEKQIGHPSPEPKEDRKVAHLT-----KPNRSRML-----EW 161
OY 65 ESSRSGHSTLSNLHRLNGELVHEKGFYYISQTYFRPQDEIKENTKNDKQWQYIY-KY 123
DB 162 EPT-YGIVLLSGVKKYKGGVLINETGLVFVYSKYVFRGQ-----SCTNLPISHKYMRN 214
OY 124 TSYPPILLMLKARNSCWSEKDAEYGLSYSTYSGIGFELKENDRIEVSVTNEHLIDMDEAS 183
DB 215 SKYPPDLYVMEKKMS-YTTTGQMAHSSYLDAVNLNTGADHLIYVNSLSLVNEESQT 273
OY 184 FFGAF 188
DB 274 FFGLY 278

RESULT 7
O9WV90 PRELIMINARY; PRT; 169 AA.
AC O9WV90;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE FAS LIGAND (FRAGMENT).
OS Marmota monax (Woodchuck).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=HEALTHY LIVER.
RC Hodgson P.D., Grant M.D., Michalak T.I.;
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
RT chronic woodchuck viral hepatitis."
RL Clin. Exp. Immunol. 0:0-0(1999).
DR EMBL; AF152368; AAD38387.1; -.
DR InterPro; IPR000478; -.
DR Pfam; PF00229; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
DR SMART; SM00207; TNF; 1.
FT NON_TER 1
FT NON_TER 169
FT NON_TER 169
SQ SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;

Query Match 17.3%; Score 172; DB 11; Length 169;
Best Local Similarity 28.4%; Pred. No. 6.5e-08;
Matches 52; Conservative 35; Mismatches 56; Indels 40; Gaps 9;

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|        |  |  |  |              |
|--------|--|--|--|--------------|
| OY     |  | 4  | RTSEETISTVBEKQONISPIVLARENCPQVAAHINGTNRSRNTLSPNSPKNKAALGRKINS  | 63           |
| Db     |  | 18                                       | INTPESTL-----EKQGHGSSPSDKALKRALRAHLT---CKPNRSRSP-----LE        | 58           |
| OY     |  | 64                                       | WESSRSGHSPLSNLHLNGLVLIHEKGYYIYSQTFRFQOEIKENTRKNDKOMVOYIY-K     | 123          |
| Db     |  | 59                                       | WEDTF-YGISILISGVAYOKGVLIVINDTGIFYEYSKRYFERGC-----SCNNQPLSHKYVK | 111          |
| OY     |  | 123                                      | YTSVPDPLLMLK-SARNSC-----WSKNAEGLVSITYGGIFELKENRIRVSYTNELHI     | 170          |
| Db     |  | 112                                      | NSKPTQDVLVLWGKKMMNYCTTGQMWAR-----SSYGAVFNFTSDHLVYNVSELILI      | 166          |
| OY     |  | 177                                      | DMD  | 179          |
| Db     |  | :  | :  | :            |
|        |  | 165                                      | NFE  | 167          |
| RESULT |  | 8  |  |              |
| O918DB |  | O918DB                                   | PRELIMINARY;   | PRT; 272 AA. |
| AC     | O918DB:  |  |  |              |
| DT     | 01-OCT-2000  | (TREMBLrel. 15                           | Created)   |              |
| DT     | 01-OCT-2000  | (TREMBLrel. 15,                          | Last sequence update)  |              |
| DT     | 01-MAR-2001  | (TREMBLrel. 16,                          | Last annotation update)  |              |
| DE     | POTATIVE CD154   | (CD40 LIGAND).                           |  |              |
| GN     | CD154.   |  |  |              |
| OS     | Gallus gallus  | (Chicken).                               |  |              |
| OC     | Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;   |  |  |              |
| OC     | Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae |  |  |              |
| CC     | Gallus.  |  |  |              |
| OX     | NCBI_TaxID=9031;   |  |  |              |
| NN     | [1]  |  |  |              |
| RP     | SEQUENCE FROM N.A.   |  |  |              |
| RC     | STRAIN-WHITE LEGHORN LINE 0; TISSUE=SPLEEN;                          |  |  |              |
| RA     | Tregaskes C.A., Young J.R., Burnside J.,                             |  |  |              |
| RL     | "cloning of a putative chicken CD40 ligand."                         |  |  |              |
| EMBL   | Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.              |  |  |              |
| DR     | InterPro; IPR000478; -   |  |  |              |
| DR     | Pfam; PF00229; TNF_1.  |  |  |              |
| DR     | PROSITE; PS00251; TNF_1; 1.  |  |  |              |
| DR     | PROSITE; PS50049; TNF_2; 1.  |  |  |              |
| SO     | SEQUENCE   | 272 AA; 30862 MW; 5409F24A8E53CD7 CRC64; |  |              |

[illegible]

GN VAS. VASCULAR ENDOTHELIAL CELL GROWTH INHIBITOR.  
OS VEGI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=VASCULAR ENDOTHELIAL;  
RA Yu G.-L., Zhai Y., Ni J., Inela-Arispe L., Huang W.-Q., Xing L.,  
RA Lu J., Kozak D., Jiang G.-W., Rojas L., Janat M.F., Bueglin M.,  
RA Gentz S., Lippman M.E., Aggarwal B.B., Ruben S., Gentz R., Li L.-Y.,  
RA Yu G.-L.;  
RT "A Novel Endothelial Cell-Specific Negative Regulator of  
RT Angiogenesis."  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF039390; AAD08783.1; -.  
DR HSSP; P01375; ATSV.  
DR InterPro: IPR000478; -.  
DR DR InterPro: IPR003636; -.  
DR Pfam: PF00229; TNEF\_1.  
DR PRINTS: PR01234; TNECROSISCF.  
DR PRODOM: PD002012; -. 1.  
DR PROSITE: PSS0049; TNEF\_2; 1.  
DR SMART: SM00207; TNEF\_1.  
SQ SEQUENCE 174 AA; 20131 MW; CCB83BA7EE673B98 CRC64;

[illegible]

RN [3]  
 SEQUENCE FROM N.A.  
 RC TISSUE-LYMPHOMA:  
 RA Force W.R., Todd P.K., Mikayama T.;  
 RT "Mouse LIGHT: Molecular Genetics, Ligand Binding and Expression."  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB029155; BAA8559.1; -  
 DR EMBL: AF123385; AAF76453.1; -  
 DR EMBL: AF227533; AAF36722.1; -  
 DR HSSP: P01375; 4TSV.  
 DR InterPro: IPR000478; -  
 DR Pfam: PF00229; TNE; 1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR PROSITE: PS50049; TNE\_2; 1.  
 SQ SEQUENCE 239 AA; 26338 MW; 217874AC71AD6BE3 CRC64;

Query Match 15.3%; Score 152.5; DB 11; Length 239;  
 Best Local Similarity 29.2%; Pred. No. 5.4e-06;  
 Matches 47; Conservative 25; Mismatches 72; Indels 17; Gaps 6;  
 QY 33 AAHTTGRGSSNTLSPNSKNEKALGRKINSWESSRSGHSLMLHNLNGELVTHEKGY 92  
 DB 93 AAHLTGANASLDIGIGP-----LIME-TRLGLAFLRGLTYHDGLVTMEPGY 139  
 QY 93 YIYQTYFRFOEIEKENTKNDKQVYIYKYTS-YPPDILMSARNSCWSKDAEYGLY 150  
 DB 140 YVYSKVQLS-GVCGPQGLANGLPITTHGLYKRTSRYPKELELVRSRSCGANSRVMWD 198  
 QY 151 SIYOGIFELKENDRIFVSVTNEHLI-DMDEASFPGAFV 190  
 DB 199 SSFLGVVHLEAGEEYVVRPGNRLVPRGRTSYFAGFV 239

RESULT 11  
 ID 070332 PRELIMINARY; PRT; 216 AA.  
 AC 070332;  
 DT 01-AUG-1998 (TREMblrel. 07, Created)  
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)  
 DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DT TUMOR NECROSIS FACTOR-ALPHA (FRAGMENT).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 NCBI\_TaxID=10036;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE-SPLEEN;  
 RA MEDLINE=98234044; PubMed=9573100;  
 RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;  
 RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and  
 RT analysis of cytokine mRNA expression in experimental visceral  
 RT leishmaniasis."  
 RL Infect. Immun. 66:2135-2142(1998).  
 DR EMBL: AF046215; AAC40100.1; -  
 DR HSSP: P06804; 2TNE.  
 DR InterPro: IPR000478; -  
 DR Pfam: PF00229; TNE; 1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR PROSITE: PS00251; TNE\_1; 1.  
 DR PROSITE: PS50049; TNE\_2; 1.  
 DR SMART: SM00207; TNE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 216 AA; 23793 MW; BADAE3F83F45B533 CRC64;

Query Match 14.5%; Score 144.5; DB 11; Length 216;  
 Best Local Similarity 26.9%; Pred. No. 2.4e-05;  
 Matches 47; Conservative 28; Mismatches 63; Indels 37; Gaps 7;

QY 28 GPOKVAH---ITGTRGRSNTL-SSPNSKNEKALGRKINS-----MESSRSGHSL 75  
 DB 49 GPQREKFPNPIITSMGQTLTLRSSQNSNDKPVGHVVAHQVEQLEMLSHRAALLN 108  
 QY 76 NLHLNGLVTHEKGYIYQTYFRFOEIEKENTKNDKQVYIYK-----YTSYPD 128  
 DB 109 GMSLKDNQVLIPADGLVLYSQVLEFRG-----CCPSVLLTHTVSRIAYSVED 157  
 QY 129 PILMSARNSCWSKDAEYG-----LSTIYOGIFELKENDRIFVSVTNEHLID 177  
 DB 158 NVNLLSAIKSPC-PKETPEGELKWPYEPYILGVFOLEKGRLSAEVNLPRYLD 211

RESULT 12  
 ID 09ERG6 PRELIMINARY; PRT; 217 AA.  
 AC 09ERG6;  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE TUMOR NECROSIS FACTOR ALPHA (FRAGMENT).  
 OS Peromyscus maniculatus (Deer mouse).  
 OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Peromyscus.  
 NCBI\_TaxID=10042;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE-SPLEEN;  
 RA Herbst M.M., Schountz T.;  
 RT "Cloning of the deer mouse interferon gamma, interleukin-10 and tumor  
 RT necrosis factor genes."  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF307013; AAG30264.1; -  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 217 AA; 23964 MW; D6F90C74C0B3021F CRC64;

Query Match 13.6%; Score 135; DB 11; Length 217;  
 Best Local Similarity 24.7%; Pred. No. 0.00017;  
 Matches 43; Conservative 35; Mismatches 72; Indels 24; Gaps 7;  
 QY 20 ISPLVBERGPPVAAHTITGTRGSSNTL-SSPNSKNEKALGRKINS-----MESSRSG 70  
 DB 48 IGPQREKFPNPLP--IIGSMAQTLTLKSSQNSDQKPAHVVAHQVDEQLEMLSRAN 105  
 QY 71 HSFLSNLHNLNGELVTHEKGYIYQTYFRFOEIEKENTKNDKQVYIYK-TSYPDP 129  
 DB 106 ALLANGMDLKNQVLIPADGLVLYSQVLEFRG-----CCSNVYLTHTVSRIAYSVEDK 160  
 QY 130 ILLMSARNSCWSKDAEYG-----LSTIYOGIFELKENDRIFVSVTNEHLID 177  
 DB 161 VNLLSAIKSPC-PKETPEGSELKWPYEPYILGVFOLEKGRLSAEVNLPRYLD 213

RESULT 13  
 ID 035853 PRELIMINARY; PRT; 232 AA.  
 AC 035853;  
 DT 01-JAN-1998 (TREMblrel. 05, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE TUMOR NECROSIS FACTOR ALPHA.  
 GN TNFA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-A/J;  
 RX MEDLINE=97246744; PubMed=9089109;

RA Iraqi F., Teale A.;  
RT Cloning and sequencing of the tufa genes of three inbred mouse  
RL strains.";  
RL Immunogenetics 45:459-461(1997).  
DB EMBL; U68414; AAB65593.1; -.  
DR HSSP; P06804; 2TNF.  
DR InterPro; IPR000478; -.  
DR InterPro; IPR003636; -.  
DR Pfam; PF00229; TNF\_1.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR PRODOM; PD00251; TNF\_1.  
DR PROSITE; PS50049; TNF\_2; 1.  
DR SMART; SM00207; TNF; 1.  
SQ SEQUENCE 232 AA; 25513 MW; 2ED6DA8E0DCAADD8 CRC64;

Query Match 13.2%; Score 131.5; DB 11; Length 232;  
Best Local Similarity 23.0%; Pred. No. 0.00038;  
Matches 41; Conservative 35; Mismatches 77; Indels 25; Gaps 7;

OY 28 GPOVAHAHTG---TRGRSNTLSSPNSKNEKALGRKINS-----WESSRGSHFLSN 76  
DB 57 GPORDEKFPNGELPGLISSMAOTLSSQNSDPYAHVANHQVEQLEMLSQANALLANG 116  
OY 77 LHLNGELVIEHKGYYIYSQYFRFOEIKENTKDKOMVOYIKYT-SYPPITLMS 135  
DB 117 MDKMDQLVVPADGLVYSQVLEKQ-----GCPDYLLTHVSRPAISYQEKVNLISA 171  
OY 136 ARNSCMSKDAEYV-----LYSIYOGIIEFLKENDRFVSYTEHLDMHKS-FPG 186  
DB 172 VKSPC-PKDTPEGAEIKPWYEPYLGIVFQLEKGDOLSAEVLNPKYLDFAESGOVYFG 228

## RESULT 14

OY1B42 PRELIMINARY; PRT; 225 AA.  
AC Q91B42;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE TUMOR NECROSIS FACTOR.  
OS Paratichthys olivaceus (Flounder).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Pleuronectoidae; Bothidae; Paralicthys.  
OC NCBI\_Taxid=8255;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hiroo I., Nam B., Kurabe T., Aoki T.;  
RT "Molecular cloning, characterization and expression of tumor necrosis  
RT factor (TNF) cDNA and gene from Japanese flounder Paralicthys  
RT olivaceus";  
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
DB EMBL; AB04048; BAA94969.1; -.  
DR InterPro; IPR000478; -.  
DR Pfam; PF00229; TNF\_1.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR PROSITE; PS50049; TNF\_2; 1.  
SQ SEQUENCE 225 AA; 24965 MW; 8F947FB25FC82658 CRC64;

Query Match 12.7%; Score 126.5; DB 13; Length 225;  
Best Local Similarity 22.0%; Pred. No. 0.001;  
Matches 42; Conservative 40; Mismatches 78; Indels 31; Gaps 8;

OY 15 EKOQNTSPVLRGPOVAHAHTGTRGRSNTLSSPNS--KNEKALGRKINSWESSRGH 71  
DB 47 EKTEPHNTLRQISSRAKAALHLEG-RDEDEETSENKLVKKNDEGLA-----FTGGGF 98  
OY 72 SFLSNLHNGELVIEHKGYYIYSQYFRFO-----EIKENTKDKOMVOY-IKYT 124

DB 99 ELVDN-----HIIIPRGLIFYSQASFRVSCSSDDADCKEAKKHLTISIRHWLFT 152  
OY 125 -SYDPDILLKMSARNSCWS-----KDAEYGLSYIYOGIIEFLKENDRFVSYTEHLID 177  
DB 153 ESLGTQVSLMSAVRSACQKQEDAYRQCGWYNAIYIGAVFQLENGKMTETINMLSELE 212  
OY 178 MDHEASFFGAF 188  
DB 213 TESGKTEFGVF 223

## RESULT 15

OY9KS8 PRELIMINARY; PRT; 205 AA.  
AC Q9UKS8;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE LYMPHOTOXIN ALPHA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OC NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,  
RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,  
RA Lasky S., Hood L.;  
RT "Sequence of the human major histocompatibility complex class III  
RT region.";  
DT Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.  
DB EMBL; AF129756; AAD18092.1; -.  
DR HSSP; P01375; 4TSV.  
DR InterPro; IPR000478; -.  
DR Pfam; PF00229; TNF\_1.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
DR SMART; SM00207; TNF; 1.  
FT VARIANT 1 M -> L.  
SQ SEQUENCE 205 AA; 22310 MW; BAOC25B7930A3A92 CRC64;

Query Match 12.3%; Score 122.5; DB 4; Length 205;  
Best Local Similarity 22.5%; Pred. No. 0.0021;  
Matches 43; Conservative 31; Mismatches 78; Indels 39; Gaps 7;

OY 9 TISTVDEKQ-----NISPLVREGRPOVAHAHTGTRGRSNTLSSPNSKNEKALGR 59  
DB 41 TPSAQTARQHPKMHLSNLKP-----AAHLIGDPSKQNSL----- 77  
OY 60 KIMSWESSRGSHFLSNLHNGELVIEHKGYYIYSQYFRFOEIKENTKDKOMVOY 119  
DB 78 ---LWRANDRAFLQDGFSLSNSLVLPTGIFYYSQVYFSKAKSPKATSSPLYLAHE 134  
OY 120 IYKVT-SYDPDILLKMSARNSCWKADEGLYSIYOGIIEFLKENDRFVSYTN-EHLID 177  
DB 135 VOLFSSQYFPHVPL-LSSQKMYVPGLQEPWLHSMYGAAAFOLTGQDOLSTHTGIPHLV- 192  
OY 178 MDHEASFFGAF 188  
DB 193 LSPSTVFFGAF 203

Search completed: October 1, 2001, 11:44:23  
Job time: 109 sec





A:Cross-references: EMBL:U11821; NID:g959430; PID:AAC50124.1; PID:g959431  
R.Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.  
Biochem. Biophys. Res. Commun. 204, 468-474, 1994

A>Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.

A:Reference number: Jc2340; MUID:95071350

A:Molecule type: DNA

A:Accession: JC2340

A:Residues: 1-281 <MT>

A:Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PID:BAA07320.1; PID:g1369902  
R.Schattelin, C.E.

A:Submitted to the EMBL Data Library, June 1995

A:Reference number: S57565

A:Accession: S57565

A>Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-281 <SC>

A:Cross-references: EMBL:X89102; NID:g887455; PID:g887456  
R.Ralston, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; G  
J. Exp. Med. 181, 71-77, 1995

A>Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.

A:Reference number: J38554; MUID:95105731

A:Accession: J38554

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-281 <RE>

A:Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628

A:Gene: FasL

A:Introns: 151/1; 116/3

A:Keywords: glycoprotein; transmembrane protein  
F:80-102/Domain: Transmembrane #Status predicted <TM>  
F:76,184,250,260/binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.1%; Score 180; DB 2; Length 281;  
Best Local Similarity 27.6%; Pred. No. 1.4e-08;  
Matches 54; Conservative 36; Mismatches 66; Indels 40; Gaps 9;

OY 3 LRTSEETISVGEKOQNT--SPLYVERGPOFVAAHITGRGRSNTLSPPNSKNEKAIGR 59  
|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 114 LRSTSQMHTASLEKQIGHPS-PPEKKELRKVAHLT--CKSNSRMP----- 159  
|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY 60 KINSMESSRSRGHSFLSNLHRLNGELVIHEKGFTYYYSQTFFPQEIEIKENTKNDKOMYOY 119  
|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 160 --LEVEDT-YGVILLISGVAKYKGGVLINETGLFYFSKYVEFGQ-----SCNNPLSLHK 210  
|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY 120 IV-KTYSYPDPPIILKKSARNS-----CWSKDAEYGLSYOGGIFELKENDRIPVSTN 172  
|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 211 VYMRNRSKTPQDYLIVMEGKMMSCTGTGMWARR-----SSYLGAVFNLSDHLTYNVSE 263  
|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY 173 EHLLDMDEHASFPGAF 188  
|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 264 LSLVNFESOSTFFGLY 279  
|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 3  
A49266  
fas ligand - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: A49266  
R:Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.  
Cell 75, 1169-1178, 1993  
A>Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor  
A:Reference number: A49266; MUID:94084792  
A:Accession: M49266  
A>Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-278 <SUD>  
A:Cross-references: GB:U03470; NID:g4440178; PIDN:AAC52129.1; PID:g4440179  
A:Keywords: glycoprotein; transmembrane protein

[illegible]

RESULT 4  
S53090  
CD40 ligand - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 05-Nov-1999  
C:Accession: S53090  
R:Martens, B.E.L.C.; Muriuki, M.  
submitted to the EMBL Data Library, February 1995  
A:Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB  
A:Reference number: S53090  
A:Accession: S53090  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-261 <MER>  
A:Cross-references: EMBL:Z48469; NID:g732569; PIDN:CA08363.1; PID:g732570

|                        |                 |                   |           |            |
|------------------------|-----------------|-------------------|-----------|------------|
| Query Match Similarity | 14.3%           | Score 142         | DB 2      | Length 261 |
| Best Local Similarity  | 27.7%           | Pred. No. 2.9e-05 |           |            |
| Matches 49             | Conservative 33 | Mismatches 69     | Indels 26 | Gaps 8     |

  

|    |     |   |     |
|----|-----|---|-----|
| QY | 13  | VOEKQONISPLTREGQPORVAHITGRSGRSTLSPNKNKALCRKINSWSSKSGHS    | 72  |
|    |     | :   | : : |
| DB | 104 | VKKKEKNPFMHGDDPQ-IAAHV-----ISBASKTTSVL-----QW-APKGY       | 146 |
|    |     | :   | : : |
| QY | 73  | FLSN--LHRLNG-ELVIEHKEGYYIYSQYFRRFOEIKENTKDXKOMOYIYKYSYDPD | 129 |
|    |     |   | : : |
| DB | 147 | TLSNMLVLTLENGQPLAVKRGQGYIYQVTCFSNRE---TLQAPEFISLKLKSPSGSE | 202 |
|    |     |   | : : |
| QY | 130 | ILMKRSARCSKSKAEKGLYISYIOGGIFELKENDRIFPVSYNENHILMDHDASFPFG | 186 |
|    |     | :   | : : |
| DB | 203 | RLLEPAANTHSSSKC--CQOSIHLGAGVELLDSGASVFNPVNDPSOVSHGCTFTSG  | 257 |
|    |     | :   | : : |

```

RESULT      5
S17289
tumor necrosis factor beta precursor - pig
C.Species: Sus scrofa domestica (domestic pig)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: S17289
R.Kühnert, P.; Wuehlrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A.Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative a
A.Reference number: S17289; MUID:91340150
A.Accession: S17289
A.Molecule type: DNA
A.Residues: 1-204 <KUN>
A.Cross-references: EMBL:X54859; NID:g2132; PIDN:CA38638.1; PID:g2133
C.Genetics:
A.Introns: 32/3; 68/1
C.Superfamily: tumor necrosis factor
C.Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage

```



Db 124 VFPDGLYLIVSOVLFFGQCPSTNFWLHTTIRIA-----VSQTKVLLSAIKSPQ 177  
 QY 142 SK-----DAEYGLYSYOGGIFELKENDRIFFSVTNEHLIDMDHEAS-FFG 186  
 Db 178 REPPEGAEAPWYEPITLVGGVFOLEKDRLSAEINLPDIYDFAESGGVYFG 228

## RESULT 8

154490

tumor necrosis factor alpha precursor - white-footed mouse

C:Species: Peromyscus leucopus (white-footed mouse)

C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 04-Feb-2000

C:Accession: I54490

R:Crew, M.D.; Filipowsky, M.E.

Immunogenetics 35, 351-353, 1992

A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leuc

A:Reference number: I54490, M0ID:92218012

A:Accession: I54490

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-235 &lt;RES&gt;

A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA0596.1; PID:g202507

C:Genetics:

A:Gene: pTNF

A:Introns: 62/3; 81/1; 97/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation

F:19/20/Binding site: myristate (lys) (covalent) #status predicted

F:84/Binding site: carboxydrate (Ser) (covalent) #status predicted

## Query Match

Best Local Similarity 13.0%; Score 129.5; DB 2; Length 235;

Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;

QY 20 ISPLVERGQRAAHTTGRGSRNLT-SSPNKNEKALGRKINSME-----SSRSGH 71

Db 56 IGQOREKKFPNNLP--TIGSMAQTTLTRSSSSQSDKPAHVAAHQVDOLEMLSGAN 113

QY 72 SFSFN-LHLNGLVLIHEKGFYIYSOTYFRFOEIKENKNDKQWQYIYK-TSPDP 129

Db 114 ALLANGLMDKNDLVIPADDLIVYSOVLEFKG-----GSSVYLTHIYSRAVSIEDK 168

QY 130 ILLKKSARNSCSKDAEYG-----LYSIYOGGIFELKENDRIFFSVTNEHLIDMDHEAS 183

Db 169 VNLISAIKSPC-EKPEPGESELPWYEPITLVGGVFOLEKDRLSAEVNLPRKYLDFAESGQ 227

QY 184 -FFG 186

Db 228 VYFG 231

RESULT 9

S21738

CD40 ligand - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 05-Nov-1999

C:Accession: S21738

R:Armstrong, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff, B.

Nature 357, 80-82, 1992

A:Title: Molecular and biological characterization of a murine ligand for CD40.

A:Reference number: S21738, M0ID:92244364

A:Accession: S21738

A:Molecule type: mRNA

A:Residues: 1-260 &lt;ARM&gt;

A:Cross-references: EMBL:X65453; NID:g50351; PIDN:CAA46448.1; PID:g50352

C:Keywords: glycoprotein; transmembrane protein

F:23-46/Domain: transmembrane #status predicted &lt;TM&gt;

F:47-260/Domain: extracellular #status predicted &lt;EXT&gt;

F:239/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 12.9%; Score 128.5; DB 2; Length 260;

Best Local Similarity 25.3%; Pred. No. 0.0046;

Matches 44; Conservative 35; Mismatches 68; Indels 27; Gaps 8;

QY 4 RTSEFTISY-----QEQQNIISPLVREGRQVRAAHTTGRGSRNLTSSPNKNEKALGR 59

Db 89 RQEDLVKDTTLNKEEKENSFEMQGDDEPQIAAHV-----VSEANSNAASVL-- 137

QY 60 KINSMESSRSGHSFSLNL-HLRNG-ELVIEHEKGFYIYSOTYFRFOEIKENKNDKQW 117

Db 138 ---QW-AKKQYIMKSLVNLVLENGKQLTVRREGIYYTYVTCNSNE-----PSSQRPFI 189

QY 118 QYIKYTSYDPDILLKKSARNSCSKDAEYGLYSYOGGIFELKENDRIFFSVT 171

Db 190 VGLMKPISGSEIRILKKAANTHSSQICEQ--QSVHLGVEFELQAGASVFNVT 241

RESULT 10

S24641

Lymphotoxin - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: I46046; S24641

R:Cludts, T.; Cleuter, Y.; Kettmann, R.; Burry, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and

A:Reference number: I46046; M0ID:94083525

A:Accession: I46046

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-204 &lt;CL2&gt;

A:Cross-references: EMBL:214137; NID:g796; PIDN:CAA78510.1; PID:g797

C:Genetics:

A:Introns: 32/3; 68/1

C:Superfamily: tumor necrosis factor

Query Match 12.8%; Score 127.5; DB 1; Length 204;

Best Local Similarity 24.9%; Pred. No. 0.0042;

Matches 47; Conservative 29; Mismatches 78; Indels 35; Gaps 9;

QY 9 TISTVQEQQNIISPLVREGRQVRAAHTT-----TRRSNTLSSPNKNEKALGRKI 61

Db 40 TPSAAPAHQQL-PTPTRTGLKPAHLVGDPSQDSLRAWT-----DRAFLR-- 88

QY 62 NSMESSRSGHSFSLNLHLRNGELVIEHEKGFYIYSOTYFRFOEIKENKNDKQWQYIY 121

Db 89 -----HGF-----SLSNSILVPTSGLYFYSSQVVFEGRCGCFPRATPTPLIAHEVQ 135

QY 122 KYT-STYDPDILLKKSARNSCSKDAEYGLYSYOGGIFELKENDRIFFSVTN- EHLIDMD 179

Db 136 LFSPOYFHVPLLSAQKSVCPGQPMV-VRSVYQAVFLLTRDQSLSTHFDGISHL-LS 193

QY 180 HEASFGAF 188

Db 194 PSSVFGAF 202

RESULT 11

JQ1344

tumor necrosis factor alpha precursor - horse

N:Alternate names: cachectin; TNF alpha

C:Species: Equus caballus (domestic horse)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C:Accession: JQ1344

R:Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosi

A:Reference number: JQ1344; M0ID:92084125

A:Accession: JQ1344

A:Molecule type: DNA

A:Residues: 1-234 &lt;SU&gt;

A:Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245



A:Residues: 1-233 <PEN>  
 A:Cross-references: GB:X02910; GB:X02159; NID:937209; PIDN:CAA26659.1; PID:937210  
 A:Note: This protein was isolated from the monocytic-like cell line HL-60 from a promyelocytic leukemia cell line.  
 R:Wang, A.M.; Cressley, A.A.; Laderer, M.B.; Lin, L.S.; Strickler, J.; Van Arsdale, J.N.; Science 228, 149-154, 1985  
 A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.  
 A:Reference number: A44189; MUID:85142190  
 A:Accession: A44189  
 A:Molecule type: mRNA  
 A:Residues: 1-62, 'S', 64-233 <WAN>  
 A:Cross-references: GB:M10988; NID:9339737; PIDN:AAA61198.1; PID:9339738  
 R:Fukuda, S.; Ando, S.; Senou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An Lymphokine Res. 7, 175-185, 1988  
 A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and A:Reference number: A61478; MUID:88301617  
 A:Accession: B61478  
 A:Molecule type: protein  
 A:Residues: 83-102;109-119;121-128, 'X',130-131;142-144, 'X',146, 'XXX',150-152;159-174;180 R:Marrenout, A.; Eransen, L.; Taverrier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima, Eur. J. Biochem. 152, 515-522, 1985  
 A:Title: Molecular cloning and expression of human tumor necrosis factor and comparison A:Reference number: 153311; MUID:86030296  
 A:Accession: 153311  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-233 <MAR>  
 A:Cross-references: GB:M26331; NID:9339763; PIDN:AAA6758.1; PID:9339764  
 A:Experimental source: U-937 cells  
 R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M. Eur. J. Biochem. 235, 431-437, 1996  
 A:Title: O-Glycosylated species of natural human tumor necrosis factor-alpha.  
 A:Reference number: S62610; MUID:96202967  
 A:Accession: S62610  
 A:Molecule type: protein  
 A:Residues: 77-99 <TAK>  
 R:D'Alfonso, S.; Richiardi, P.M. Immunogenetics 39, 150-154, 1994  
 A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter region A:Reference number: 154522; MUID:94102809  
 A:Accession: 154522  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-8 <DAL>  
 A:Cross-references: GB:S68530; NID:9544751  
 R:Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H. J. Exp. Med. 176, 1053-1062, 1992  
 A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lys A:Reference number: A59163; MUID:93018820  
 A:Accession: A59163  
 A:Contents: annotation, identification of myristylated lysines  
 R:Aggarwal, B.B.; Kohrt, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bring J. Biol. Chem. 260, 2345-2354, 1985  
 A:Title: Human tumor necrosis factor. Production, purification, and characterization. A:Reference number: A92511; MUID:85130974  
 A:Accession: A92511  
 A:Contents: annotation, disulfide bond  
 C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction out detriment to normal cells. It can also act synergistically with interferon gamma to C:Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely ut are produced by different cell types and have different induction kinetics.  
 C:Genetics:  
 A:Gene: GDB:TNF; TNFA  
 A:Cross-references: GDB:120441; OMIM:191160  
 A:Map position: 6p21.3-6p21.3  
 A:Introns: 62/3; 78/1; 94/1  
 C:Complex: homotrimer  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macro F:1-76/Domain: propeptide #status predicted <PRO>  
 F:77-233/Product: tumor necrosis factor #status experimental <MAT>  
 F:19,20/Binding site: myristate (Lys) (covalent) #status experimental  
 F:81/Binding site: carboxylate (Ser) (covalent) (partial) #status experimental  
 F:145-177/Disulfide bonds: #status experimental

Query Match 12.3%; Score 123; DB 1; Length 233;  
 Best local similarity 23.0%; Pred. No. 0.0012;  
 Matches 43; Conservative 32; Mismatches 70; Indels 42; Gaps 8;  
 QY 28 GPCR-----VAHITGRGRSNTLSSPNSK-----NEKALGRKINSMESSRSCH 71  
 DB 57 GPQREFPPDLSLISPLAQAAYRSSRT---PSDKPAHVAVNPAQAGOL--OMLNRRANA 111  
 QY 72 SFLSNLRLNGELVIEKGFYYSOTYFPEFEIKENTKNDKQWQYLYKKT-----S 125  
 DB 112 LLANGVELNDQLVYSEGLYLYSOYLEKQ-----GCPSTHVLTHTRISIAAS 162  
 QY 126 YPDPIILMKSARNCSWCK----DAEYGLYSYQGIPELKEKNDRIEVSVTNEHLIDMH 180  
 DB 163 YQTKVNLISAISPCQREFPEGAERKPEYELIGVQLEKGRLSAEINRPDYIDFAE 222  
 QY 181 EAS-FRG 186  
 DB 223 SGOVYFG 229

## RESULT 14

## OMRUX

Lymphotoxin alpha precursor - human  
 N:Alternate names: Lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta)  
 C:Species: Homo sapiens (man)  
 C:Date: 28-Aug-1985 #sequence, revision 07-Jul-1995 #text, change 16-Jun-2000  
 C:Accession: A92755; S36154; 154482; A93350; B32877; A91906; A61478; S26951; A01645;  
 J. Nedwin, G.E.; Jarrett-Nedwin, J.; Smith, D.H.; Naylor, S.L.; Sakaguchi, A.Y.; Goed J. Cell. Biochem. 29, 171-181, 1985  
 A:Title: Structure and chromosomal localization of the human lymphotoxin gene.  
 A:Reference number: A92755; MUID:86086150  
 A:Accession: A92755  
 A:Molecule type: DNA  
 A:Residues: 1-59, 'N', 61-205 <NED>  
 R:Riris, F.J.M.; Bougueleret, L.; Prieur, S.; Catherine, D.; Primas, G.; Perrot, V.; Ju Nature Genet. 3, 137-145, 1993  
 A:Title: Dense Alu clustering and a potential new member of the NFkappaB family withl A:Reference number: S36152; MUID:93272029  
 A:Accession: S36154  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-12, 'R', 14-205 <IRT>  
 A:Cross-references: EMBL:Z15026; NID:937211; PIDN:CAA78746.1; PID:937213  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992  
 R:Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S. Immunogenetics 33, 50-53, 1991  
 A:Title: Haplotypic polymorphisms of the TNFB gene.  
 A:Reference number: 154482; MUID:91139175  
 A:Accession: 154482  
 A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-124, 'P', 126-205 <RES>  
 A:Cross-references: GB:M55913; NID:9339742; PIDN:AAB59455.1; PID:9339743  
 A:Experimental source: ancestral haplotype 57.1  
 A:Note: 59-Asn was also found (ancestral haplotype 8.1)  
 R:Gray, P.W.; Aggarwal, B.B.; Benton, C.V.; Bringman, T.S.; Henzel, W.J.; Jarrett, J. Nature 312, 721-724, 1984  
 A:Title: Cloning and expression of cDNA for human lymphotoxin, a lymphokine with tumo A:Reference number: A93350; MUID:85086243  
 A:Accession: A93350  
 A:Molecule type: mRNA  
 A:Residues: 1-205 <GRA>  
 A:Cross-references: GB:X01393; NID:934444; PIDN:CAA25649.1; PID:934445  
 A:Experimental source: lymphoblastoid cell line RPMI-1788  
 R:Goeddel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Palladino, M. Cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986  
 A:Title: Tumor necrosis factors: gene structure and biological activities.  
 A:Reference number: A32877; MUID:87217059  
 A:Accession: B32877  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 35-205 <GDE>

A>Title: Cloning and expression of human lymphotoxin mRNA derived from a human T cell hybridoma  
A.Reference number: A91906; MUID:87051135

A:Molecule type: mRNA  
A.Residues: 1-59,'N','61'-205 <KOB>  
A:CROSS-references: GB:D00102; NID:g219913; PIDN:BAA00064.1; PIR:g219914

A>Note: The authors translated the codon TAT for residue 156 as Thr and ACC for residue R.Fukuda, S.; Ando, S.; Sanou, O.; Tanaka, W.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An Lymphokine Res., 7, 175-185, 1988

A>Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and A.Reference number: A61478; MUID:88301617

A:Molecule type: protein  
A.Residues: 56-79;86-95,'X','97','X','99',119-151,'XX',154-162,'X',164,'X',166,'X',168,'X',1 R.Voigt, C.G.; Maurer-Fogy, I.; Adolf, G.R.  
FEBS Lett. 314, 85-88, 1992

A>Title: Natural human tumor necrosis factor beta (Lymphotoxin). Variable O-glycosylated A.Reference number: S26951; MUID:93083656

A:Accession: S26951  
A:Molecule type: protein  
A.Residues: 35-59,'N','61'-205 <VOI>  
A>Note: 60-Thr was also found  
R.Fukushima, K.; Watanabe, H.; Takeoe, K.; Nomura, M.; Asahi, T.; Yamashita, K.

Arch. Biochem. Biophys. 304, 144-153, 1993

A>Title: N-linked sugar chain structure of recombinant human lymphotoxin produced by CHO A.Reference number: S34742; MUID:93311995

A:Contents: annotation  
C:Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction, while having no detrimental effect on normal cells. It can also act synergistically with C:Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of different local activities but are produced by different cell types and have different induction k4 Genetics:

A:Gene: GDB:LTA; LT; TNFB  
A:Cross-references: GDB:120442; OMIM:153440

A:Map position: 6p21.3-6p21.3

A:Introns: 33/3; 69/1  
A>Note: the first intron occurs before the initiator codon  
C:Superfamily: tumor necrosis factor  
C:Keywords: cytokine; cytotoxicity; glycoprotein; homotrimer; lymphokine; macrophage F:1-34/DNA: signal sequence #status predicted <SIG>

F:35-205/Product: lymphotoxin #status predicted <MAT>  
F:41/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental  
F:96/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 12.2%; Score 122; DB 1; Length 205;  
Best Local Similarity 23.4%; Pred. No. 0.0013;  
Matches 37; Conservative 29; Mismatches 72; Indels 20; Gaps 5;

OY 33 AAHTGTGRTGRNTTSSPSKNKEALGKRINSGESRSQHSPLSNLHNGELVTHKEGFY 92  
||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 64 AAHLIGDSKNSL-----LMKANTDRAFLQDGFSLSNNSLVLPTSGIT 107

OY 93 YIVSQTYFRFOEIKENTKNDKOMQVLYTKYT-SYPEDILMKSRANSCKDAEGDYLS 151  
::: || | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 108 FYVSQQWVESGAKAEPKATSSPLYLAHEVOLFFRSSQVPFHVPLL-SSQKWVYGGLDEPWLHS 166

OY 152 IVGGCIFETAKENDRFYSVTN-EHLIDMDHEASFPFGAF 188  
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 167 MYHGAAPOLTGCDOLSTHTTDGIPIHLV-LSPSTVEFGAF 203

RESULT 15

OMMSN  
tumor necrosis factor alpha precursor - mouse  
N:Alternate names: cachectin; TNF alpha  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 04-Feb-2000  
R:Accession: A22908; S03791; A27303; A25164; A23127; I59058; A36696  
R:Shihata, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.  
DNA 7, 193-201, 1988

A>Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necro A.Reference number: A22908; MUID:88224564

A:Accession: A22908  
A:Molecule type: DNA  
A.Residues: 1-235 <SHI>  
A:CROSS-references: GB:M20155  
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A:Molecule type: DNA  
A.Residues: 1-235 <SHA>  
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A:Accession: A27303  
A:Molecule type: DNA  
A.Residues: 1-235 <SEM>  
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A:Accession: A25164  
A:Molecule type: mRNA  
A.Residues: 1-235 <PEN>  
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A:Accession: A23127  
A:Molecule type: mRNA  
A.Residues: 1-235 <FRA>  
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A>Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide resul A.Reference number: A34251; MUID:89380231

A:Accession: A34251  
A:Molecule type: protein  
A.Residues: 70-87 <CSE>  
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A>Title: Identification of a common nucleotide sequence in the 3'-untranslated region A.Reference number: I59058; MUID:86149365

A:Accession: I59058  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A.Residues: 1-230,'R',232-235 <RES>  
A:CROSS-references: GB:M13049; NID:g202082; PIDN:AAA0457.1; PID:g202083  
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A>Title: Characterization of high molecular weight glycosylated forms of murine tumor A.Reference number: A36696; MUID:91097531

A:Accession: A36696  
A:Molecule type: protein  
A.Residues: 80-85,'X',87-99 <SHE>  
C:Genetics:  
A:Note: the first intron occurs in the 5'-untranslated region  
C:Superfamily: tumor necrosis factor  
C:Keywords: cytokine; cytotoxicity; glycoprotein; lipoprotein; lymphokine; macrophage; m F:80-235/Product: tumor necrosis factor #status experimental <MAT>  
F:84/Binding site: myristate (lys) (covalent) #status predicted  
F:86/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F:148-179/disulfide bonds: #status predicted

